Figure 1

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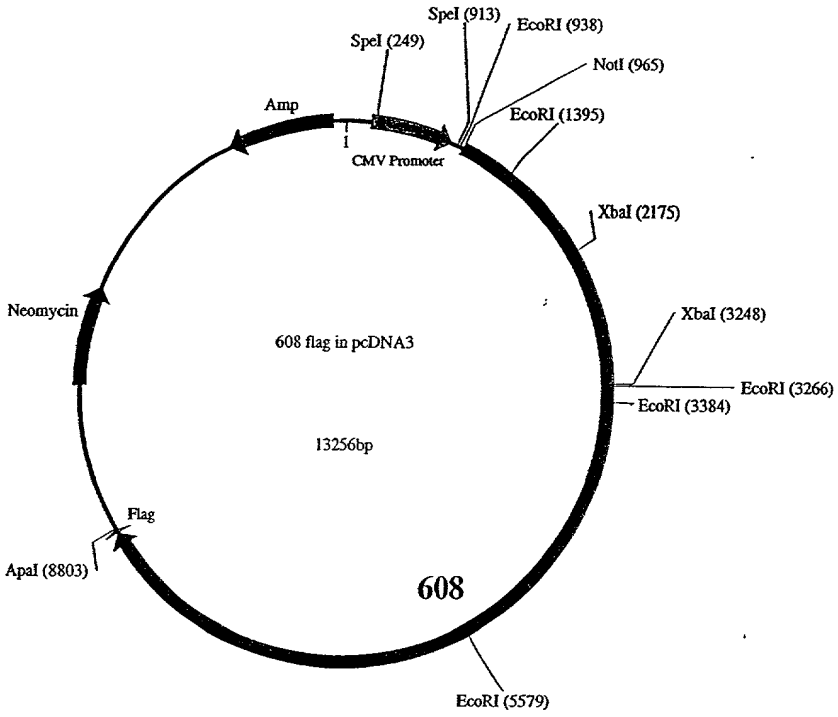
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Figure 3

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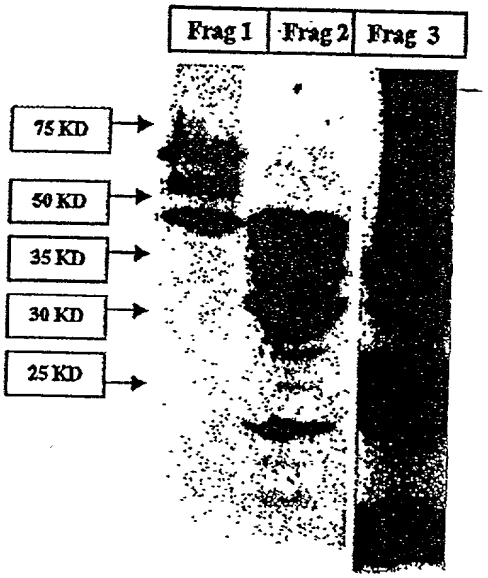

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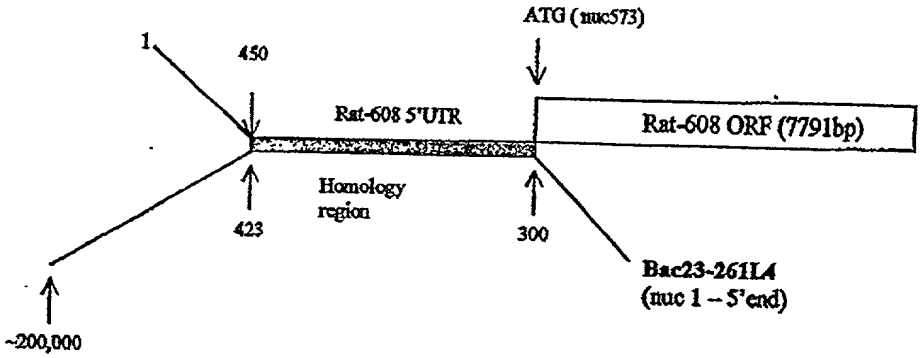

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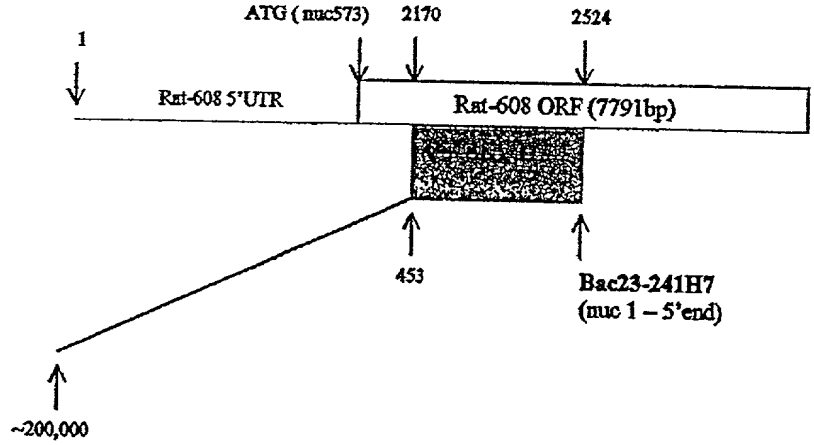

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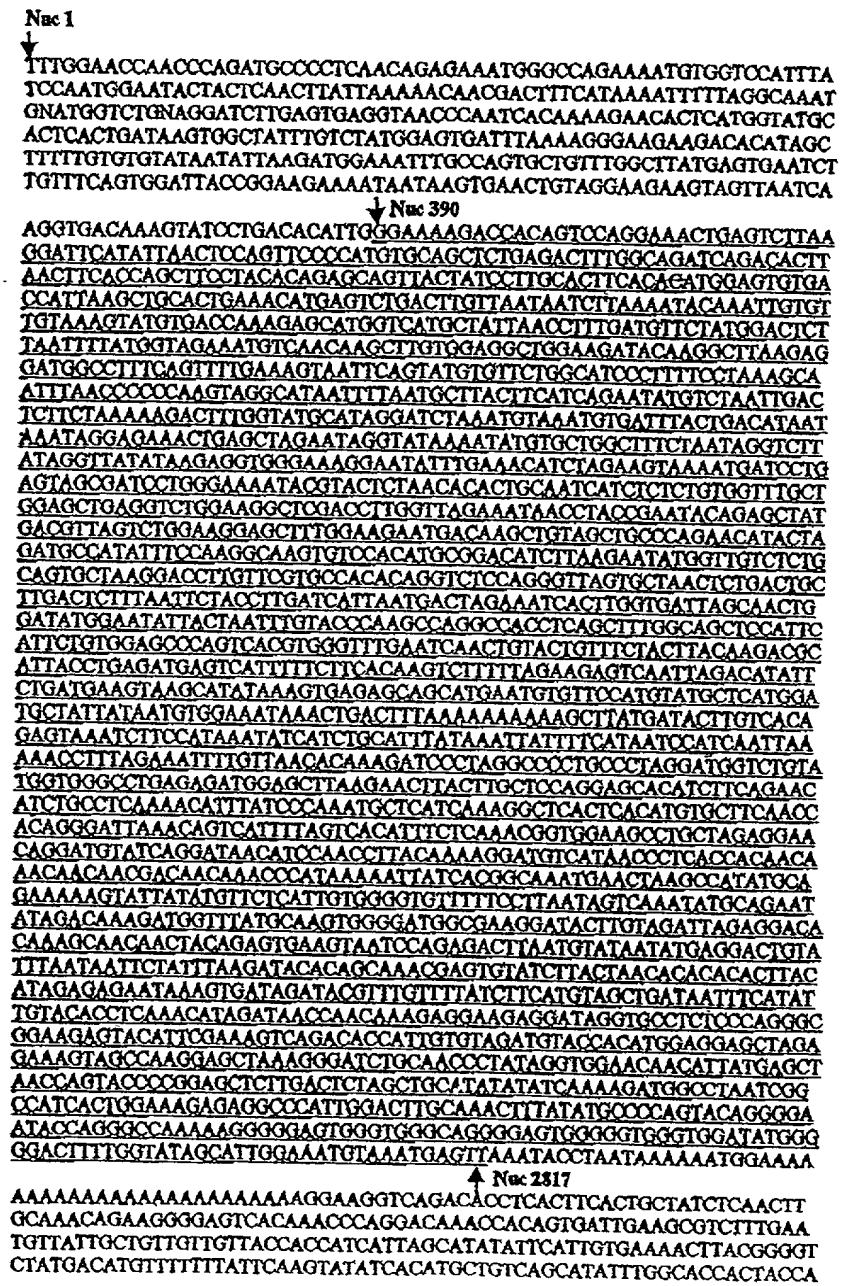

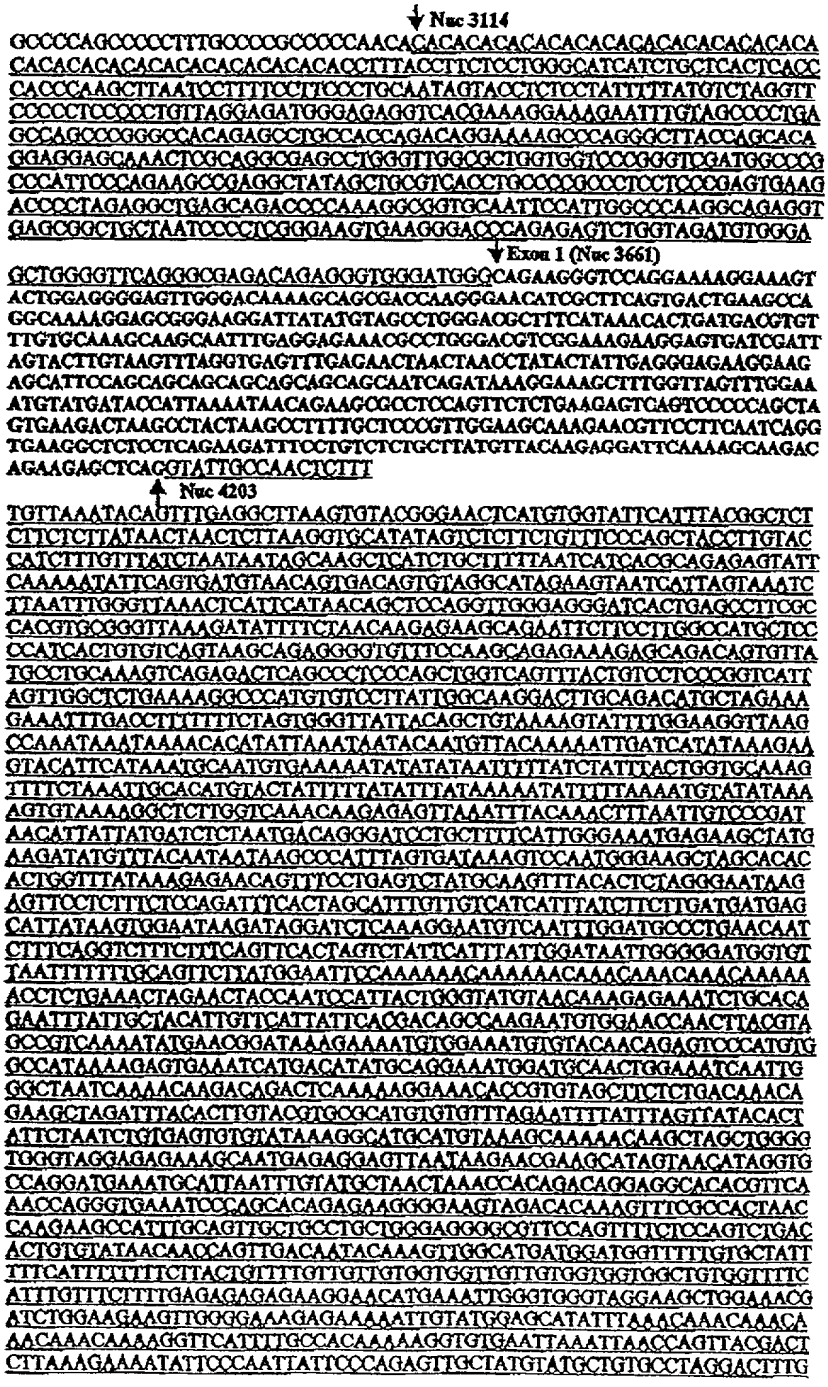
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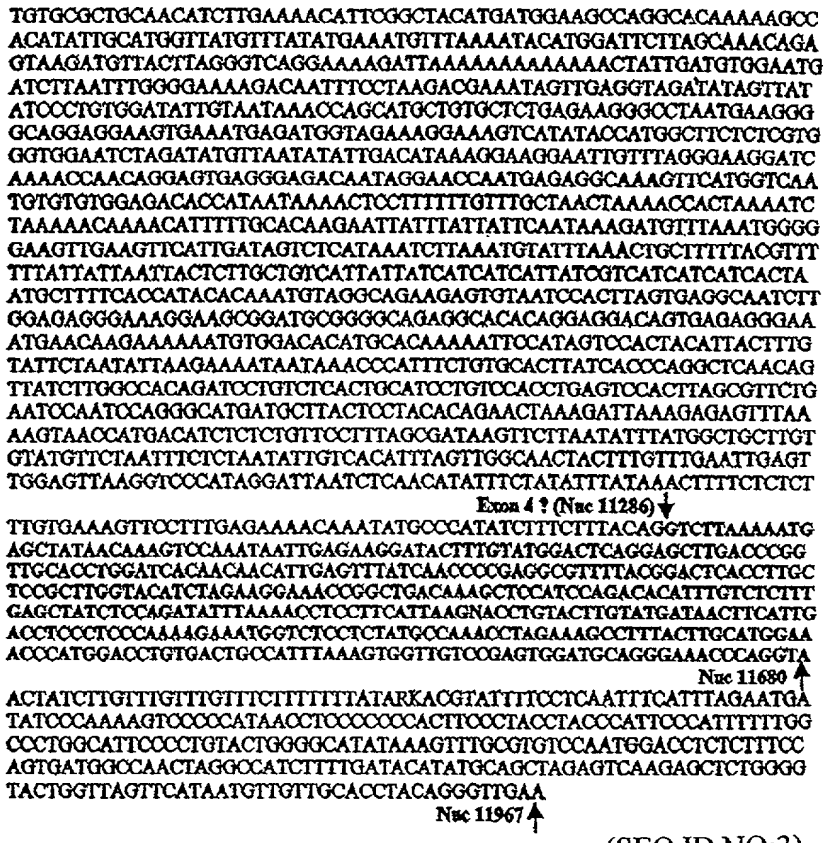

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Figure 8

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Figure 9

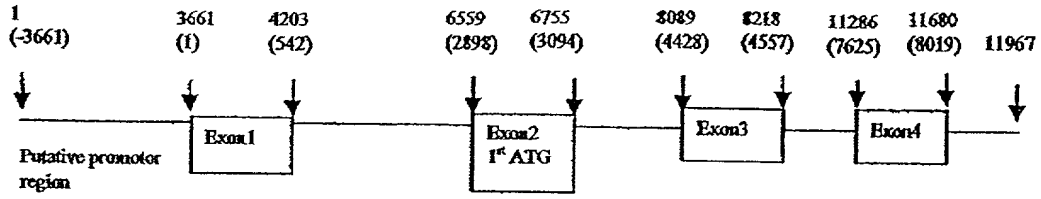
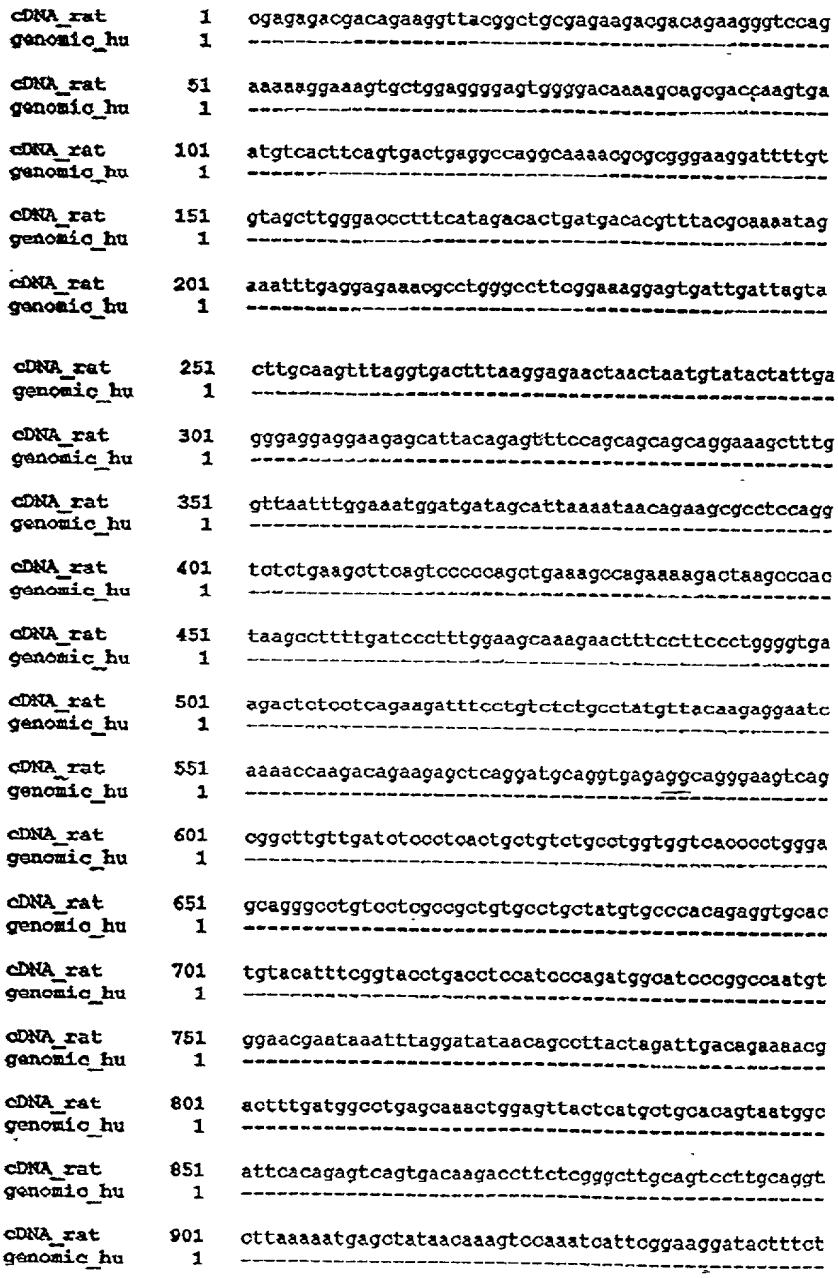


Figure 10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cDNA_rat      951   acggactcgggagcttggtccggttgcacctggatcacaacaacattgaa
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1001   ttcatcaaccctgaggccttttatggacttacctcgctccgcttggtaca
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1051   tttagaaggaaaccggctcacaaagctccatccagacacatttgtctcat
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1101   taagctatctccagatatttaaaacctctttcattaagtacctgttcttg
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1151   tctgataacttcctgacctccctccccaaaagaaatggtctcctacatgcc
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1201   aaacctagaaagcctgtatttgcatggaaacccatggacctgtgactgcc
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1251   atttaaagtggttgtctgagtggatgcagggaaacccagatataataaaa
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1301   tgcaagaaagacagaagctcttccagtcctcagcaatgtccccctttgcat
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1351   gaaccccaggatctctaaaggcagacccctttgctatggtaccatctggag
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1401   ctttcctatgtacaaagccaaccattgatccatcactgaagtcaaagagc
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1451   ctggttactcaggaggacaatggatctgcctccacctcacctcaagattt
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1501   catagaaccctttggctccttgtctttgaacatgacananntntctggaa
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1551   ataaggccgacatggtctgtagtatccaaaagccatcaaggacatcacca
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1601   actgcattcactgaagaaaatgactacatcatgctaaatgcgtcattttc
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1651   cacaaatcttgtgtgcagtgtagattataatcacatccagccagtgtggc
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1701   aacttctggctttatacagtgactctcctctgatactagaaaggaagccc
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1751   cagcttaccgagactccttcactgtcttctagatataaacaggtggctct
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1801   taggcctgaagacatttttaccagcatagaggctgatgtcagagcagacc
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1851   ctttttggttccaacaagaaaaaattgtcttgcagctgaacagaactgcc
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1901   accacacttagcacattacagatccagttttccactgatgctcaaatcgc
genomic_hu      1   ----------------------------------------------------

cDNA_rat     1951   tttaccaagggcggagatgagagcggagagactcaaatggaccatgatcc
genomic_hu      1   ----------------------------------------------------
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cDNA_rat      2001   tgatgatgaacaatcccaaactggaacgcactgtcctggttggcggcact
genomic_hu       1   --------------------------------------------------

cDNA_rat      2051   attgccctgagctgtccaggcaaaggcgacccttcacctcacttggaatg
genomic_hu       1   --------------------------------------------------

cDNA_rat      2101   gcttctagctgatgggagtaaagtgagagccccttacgttagcgaggatg
genomic_hu       1   --------------------------------------------------

cDNA_rat      2151   ggcgaatcctaatagacaaaaatgggaagttggaactgcagatggctgac
genomic_hu       1   --------------------------------------------------

cDNA_rat      2201   agctttgatgcaggtctttaccactgcataagcaccaatgatgcagatgc
genomic_hu       1   --------------------------------------------------

cDNA_rat      2251   ggatgttctcacatacaggataactgtggtagagccctatggagaaagca
genomic_hu       1   --------------------------------------------------

cDNA_rat      2301   cacatgacagtggagtccagcacacagtggttacgggtgagacgctcgac
genomic_hu       1   --------------------------------------------------

cDNA_rat      2351   cttccatgcctttccacgggtgttccagatgcttctattagctggattct
genomic_hu       1   --------------------------------------------------

cDNA_rat      2401   tccagggaacactgtgttctctcagccatcaagagacaggcaaattctta
genomic_hu       1   --------------------------------------------------

cDNA_rat      2451   acaatgggaccttaagaatattacaggttacgccaaaagatcaaggtcat
genomic_hu       1   --------------------------------------------------

cDNA_rat      2501   taccaatgtgtggctgccaacccatcaggggccgacttttccagttttaa
genomic_hu       1   --------------------------------------------------

cDNA_rat      2551   agtttcagttcaaaagaaaggccaaaggatggttgagcatgacagggagg
genomic_hu       1   --------------------------------------------------

cDNA_rat      2601   caggtggatctggacttggagaacccaactccagtgtttcccttaagcag
genomic_hu       1   --------------------------------------------------

cDNA_rat      2651   ccagcatctttgaaactctctgcatcagctttgacagggtcagaggctgg
genomic_hu       1   --------------------------------------------------

cDNA_rat      2701   aaaacaagtctccggtgtacataggaagaacaaacatagagacttaatac
genomic_hu       1   --------------------------------------------------

cDNA_rat      2751   atcggcggcgtggggattccacgctccggcgattcagggagcataggagg
genomic_hu       1   --------------------------------------------------

cDNA_rat      2801   cagctccctctctctgctcggagaattgacccgcaacgctgggcagcact
genomic_hu       1   --------------------------------------------------

cDNA_rat      2851   tctagaaaaagccaaaaagaattctgtgccaaaaaagcaagaaaatacca
genomic_hu       1   --------------------------------------------------

cDNA_rat      2901   cagtaaagccagtgccactggctgttcccctcgtggaactcactgacgag
genomic_hu       1   --------------------------------------------------

cDNA_rat      2951   gaaaaggatgcctctggcatgattcctccagatgaagaattcatggttct
genomic_hu       1   --------------------------------------------------
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cDNA_rat      3001  gaaaactaaggcttctggtgtcccaggaaggtcaccaactgctgactctg
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3051  gaccagtaaatcatggttttatgacgagtatagcttctggcacagaagtc
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3101  tcaactgtgaatccacaaacactacaatctgagcaccttcctgatttcaa
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3151  attatttagtgtaacaaacggtacagctgtgacaaagagtatgaacccat
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3201  ccatagcaagcaaaatagaagatacaaccaaccaaaaacccaatcattatc
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3251  tttccatcagtagctgaaattcgagattctgctcaggcaggaagagcatc
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3301  ttcccaaagtgcacacctgtaacaggggaaacatggctacctatggcc
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3351  ataccaacacatatagtagctttaccagcaaagccagtacagtcttgcag
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3401  ccaataaatccaacagaaagttatggacctcagatacctattacaggagt
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3451  cagcagacctagcagtagtgacatctcttctcacactactgcagacccta
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3501  gcttctccagtcacccttcaggttcacacaccactgcctcgtctttattt
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3551  cacattcctagaaacaacaatacaggtaacttcccottgtccaggcactt
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3601  gggaagagagaggacaatttggagcagagggagagttaaaaacccacata
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3651  gaaccccagttctccgacggcatagacacaggactgtgaggccagcaatc
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3701  aagggacctgctaacaaaaatgtgagccaagttccagccacagagtacca
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3751  tgggatgtgccacacatgtccttccgcagaggggctcacagtggctactg
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3801  cagcactgtcagttccaagttcatcccacaagtgcctccccaaaactaat
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3851  aatgttggggtcatagcagaagagtctaccactgtggtcaagaaaccact
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3901  gttactatttaaggacaaacaaaatgtagatattgagataataacaacca
genomic_hu       1  ----------------------------------------------------

cDNA_rat      3951  ctacaaaatattccggaggggaaagtaaccacgtgattcctacggaagca
genomic_hu       1  ----------------------------------------------------

cDNA_rat      4001  agcatgacttctgctccaacatctgtatccctggggaaatctcctgtaga
genomic_hu       1  ----------------------------------------------------

cDNA_rat      4051  caatagtggtcacctgagcatgcctgggaccatccaaactgggaaagatt
genomic_hu       1  ----------------------------------------------------

cDNA_rat      4101  cagtggaaacaacaccacttcccagcccccctcagcacaccctcaatacca
genomic_hu       1  ----------------------------------------------------
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cDNA_rat      4151  acaagcacaaaattctcaaagaggaaaactcccttgcaccagatctttgt
genomic_hu       1  ------------------------------------------------

cDNA_rat      4201  aaataaccagaagaaggagggatgttaaagaatccatatcaattcggtt
genomic_hu       1  ------------------------------------------------

cDNA_rat      4251  tacaaaagaacccagccgcaaagcttcccaaaatagctcctcttttaccc
genomic_hu       1  ------------------------------------------------

cDNA_rat      4301  acaggtcagagttcccccctcagattctacaactctcttgacaagtccgcc
genomic_hu       1  ------------------------------------------------

cDNA_rat      4351  accagctctgtctacaacaatggctgccactcagaacaagggcactgaag
genomic_hu       1  ------------------------------------------------

cDNA_rat      4401  tagtatcaggtgccagaagtctctcagcagggaagaagcagcccttcacc
genomic_hu       1  ------------------------------------------------

cDNA_rat      4451  aactcctctccagtgcttcctagcaccataagcaagagatctaatacatt
genomic_hu       1  ------------------------------------------------

cDNA_rat      4501  aaacttcttgtcaacggaaaccccccacagtgacaagtcctactgctactg
genomic_hu       1  ------------------------------------------------

cDNA_rat      4551  catctgtcattatgtctgaaacccaacgaacaagatccaaagaagcaaaa
genomic_hu       1  ------------------------------------------------

cDNA_rat      4601  gaccaaataaaggggcctcggaagaacagaaacaacgcaaacaccacccc
genomic_hu       1  ------------------------------------------------

cDNA_rat      4651  caggcaggtttctggctatagtgcatactcagctctaacaacagctgata
genomic_hu       1  ------------------------------------------------

cDNA_rat      4701  ccccttggctttcagtcattccccacgacaagatgatggtggaaatgta
genomic_hu       1  ------------------------------------------------

cDNA_rat      4751  agtgcagttgcttatcactcaacaacctctcttctggccataactgaact
genomic_hu       1  ------------------------------------------------

cDNA_rat      4801  gtttgagaagtacacccagactttgggaaatacaacagctttggaaacaa
genomic_hu       1  ------------------------------------------------

cDNA_rat      4851  cgttgttgagcaaatcacaggagagtaccacagtgaaaagagcctcagac
genomic_hu       1  ------------------------------------------------

cDNA_rat      4901  acaccaccaccactcctcagcagtggggcgcccccagtgcccactccttc
genomic_hu       1  ------------------------------------------------

cDNA_rat      4951  cccacctcctttactaagggtgtggttacagacagcaaagtcacatcag
genomic_hu       1  ------------------------------------------------

cDNA_rat      5001  ctttccagatgacgtcaaatagagtggtcaccatatatgaatcttcaagg
genomic_hu       1  ------------------------------------------------

cDNA_rat      5051  cacaatacagatctgcagcaaccctcagcagaggctagccccaatcctga
genomic_hu       1  ------------------------------------------------

cDNA_rat      5101  gatcataactggaaccactgactctccctctaatctgtttccatccactt
genomic_hu       1  ------------------------------------------------

cDNA_rat      5151  ctgtgccagcactaagggtagataaaccacagaattctaaatggaagccc
genomic_hu       1  ------------------------------------------------

cDNA_rat      5201  tctccctggccagaacacaaatatcagctcaagtcatactccgaaaccat
genomic_hu       1  ------------------------------------------------
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cDNA_rat      5251   tgagaagggcaaaaggccagcagtaagcatgtccccccacctcagccttc
genomic_hu       1   ------------------------------------------------

cDNA_rat      5301   cagaggccagcactcatgcctcacactggaatacacagaagcatgcagaa
genomic_hu       1   ------------------------------------------------

cDNA_rat      5351   aagagtgtttttgataagaaacctggtcaaaaccccaacttccaaacatct
genomic_hu       1   ------------------------------------------------

cDNA_rat      5401   gccttacgtctctctacctaagactctattgaaaaagccaagaataattg
genomic_hu       1   ------------------------------------------------

cDNA_rat      5451   gaggaaaggctgcaagctttacagttccagctaattcagaogttttttctt
genomic_hu       1   ------------------------------------------------

cDNA_rat      5501   ccttgtgaggctgttggagacccactgcccatcatccactggaccagagt
genomic_hu       1   ------------------------------------------------

cDNA_rat      5551   ttcatcaggatttgaaatatcccaagggacacagaaaagccggttccacg
genomic_hu       1   ------------------------------------------------

cDNA_rat      5601   tgcttcccaatggcaccttgtccatccagagggtcagtattcaggaccgt
genomic_hu       1   ------------------------------------------------

cDNA_rat      5651   ggacagtacctgtgctctgcatttaatccactgggcgtagaccattttca
genomic_hu       1   ------------------------------------------------

cDNA_rat      5701   tgtctctttgtctgtggtttttacccggcaaggattttggacagacatg
genomic_hu       1   ------------------------------------------------

cDNA_rat      5751   tcaaggagatcacagttcactttggaagtactgtggaactaaagtgcaga
genomic_hu       1   ------------------------------------------------

cDNA_rat      5801   gtggagggtatgccgaggcctacggtttcctggatacttgcaaaccaaac
genomic_hu       1   ------------------------------------------------

cDNA_rat      5851   ggtggtctcagaaacggccaagggaagcagaaaggtctgggtaacacctg
genomic_hu       1   ------------------------------------------------

cDNA_rat      5901   atggaacattgatcatctataatctgagtctttatgatcgtggtttttac
genomic_hu       1   ------------------------------------------------

cDNA_rat      5951   aagtgtgtggccagcaacccatctggccaggattcactgttggttaagat
genomic_hu       1   ------------------------------------------------

cDNA_rat      6001   acaagtcatcacagctccccctgtcattatagagcaaaagaggcaagcca
genomic_hu       1   ------------------------------------------------

cDNA_rat      6051   tcgttggggttttaggtggaagtttgaaactgccctgcactgcaaaagga
genomic_hu       1   ------------------------------------------------

cDNA_rat      6101   actccccagcctagtgttcactgggtcctttatgatgggactgaactaaa
genomic_hu       1   ------------------------------------------------

cDNA_rat      6151   accattgcagttgactcattccagatttttcttgtatccaaatggaactc
genomic_hu       1   ------------------------------------------------

cDNA_rat      6201   tgtatataagaagcatcgctccttcagtgaggggcacttatgagtgcatt
genomic_hu       1   ------------------------------------------------

cDNA_rat      6251   gccaccagctcctcaggctcagagagaagggtagtgattcttactgtgga
genomic_hu       1   ------------------------------------------------
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cDNA_rat      6301   agagggagagacaatccccaggatagaaactgcctctcagaaatggactg
genomic_hu       1   ------------------------------------------------------

cDNA_rat      6351   aggtgaatttgggtgagaaattactactgaactgctcagctactggggat
genomic_hu       1   ------------------------------------------------------

cDNA_rat      6401   ccaaagcctagaataatctggaggctgccatccaaggctgtcatcgacca
genomic_hu       1   ------------------------------------------------------

cDNA_rat      6451   gtggcacagaaTGGGCAGCCGAATCCACGTCTACCCAAATGGATCCTTGg
genomic_hu       1   -----------TGGGCAGCTGGATCCACGTCTACCCTAATGGATCCCTGt

cDNA_rat      6501   tggttgggTCAGTGACGGAAAAAGACGCTGGTGACTACTTATGTGTGGCA
genomic_hu      40   ttattggaTCAGTAACAGAAAAAGACAGTGGTGTCTACTTGTGTGTGGCA

cDNA_rat      6551   AGAAACAAAATGGGAGATGACCTAGTCCTGATGCATGTccgcctgAGATT
genomic_hu      90   AGAAACAAAATGGGGGATGATCTGATACTGATGCATGTtagcctaAGACT

cDNA_rat      6601   GACACCTGCCAAAATTGAACAGAAGCAGTATTTTAagAAGCAAGTGCTCC
genomic_hu     140   GAAACCTGCCAAAATTGACCACAAGCAGTATTTTAgaAAGCAAGTGCTCC

cDNA_rat      6651   ATGGGAAAGATTTCCAAGTTGACTGCAaggcctctGGCTCCCCTGTGCCT
genomic_hu     190   ATGGGAAAGATTTCCAAGTAGATTGCAaagcttccGGCTCCCCAGTGCCA

cDNA_rat      6701   GAGGTATCCTGGAGTTTGCCTGATGggacagtgcTCAACAATGTAGCCCA
genomic_hu     240   GAGATATCTTGGAGTTTGCCTGATGgaaccatgaTCAACAATGCAATGCA

cDNA_rat      6751   AGCTGATGACAGTGGCTATAGGACcaagaggtacACCCTTTTCCACAATG
genomic_hu     290   AGCCGATGACAGTGGCCACAGGACtaggagatatACCCTTTTCAACAATG

cDNA_rat      6801   GAACCTTGTATTTCAACAACGTTGggatggcaGAGGAAGGAGATTATATC
genomic_hu     340   GAACTTTATACTTCAACAAAGTTGgggtagcgGAGGAAGGAGATTATACT

cDNA_rat      6851   TGCTCTGCCCAGAACACCTTAGGGAAAGATGAGATGAAAGTCCACCTAAC
genomic_hu     390   TGCTATGCCCAGAACACCCTAGGGAAAGATGAAATGAAGGTCCACTTAAC

cDNA_rat      6901   AGTTCTAACAGCcatcCCACGGATAAGGCAAAGCTACAAGACCACCATGA
genomic_hu     440   AGTTATAACAGCtgctCCCCGGATAAGGCAGAGTAACAAAACCAACAAGA

cDNA_rat      6951   GGCTCAggGCTGGAGAAACAGCTGTCCTTGACTGCGAGGTCACTGGGGaa
genomic_hu     490   GAATCAaaGCTGGAGACACAGCTGTCCTTGACTGTGAGGTCACTGGGGat

cDNA_rat      7001   ccgaagcccaatgTATTTTGGTTGCTGCCTTCCAAcaatgtcATTTCATT
genomic_hu     540   cccaaaccaaaaaTATTTTGGTTGCTGCCTTCCAATgacatgATTTCCTT

cDNA_rat      7051   CTCCAATGACAGGTTCACATTTCATGCCAATagaaCTTTGTCCATCCATA
genomic_hu     590   CTCCATTGATAGGTACACATTTCATGCCAATgggtCTTTGACCATCAACA

cDNA_rat      7101   AAGTGAAACCACTTGACTCTGGGGActatgtgtgcgtagctcagAATCCT
genomic_hu     640   AAGTGAAACTGCTCGATTCTGGAGAgtacgtatgtgtagcccgaAATCCC

cDNA_rat      7151   AGTGGGGATGACACTAAGACATACAAACTGGAcattGTCTCTAAACCTCC
genomic_hu     690   AGTGGGGATGACACCAAAATGTACAAACTGGAtgtgGTCTCTAAACCTCC

cDNA_rat      7201   ATTAATCAATGGCCTGTATGCAAACAagACTGTTATTAAAGCCACAGCca
genomic_hu     740   ATTAATCAATGGTCTGTATACAAACAgaACTGTTATTAAAGCCACAGCtg

cDNA_rat      7251   ttcggcacTCCAAAAAATACTTTGACTGCAGAGCAGATGGGATCCCATct
genomic_hu     790   tgagacatTCCAAAAAACACTTTGACTGCAGAGCTGAAGGGACACCATct

cDNA_rat      7301   tcccaggtcacGTGGATTATGCCAGGCAATATTTTCCTCCCAGCTCCATA
genomic_hu     840   cctgaagtcatGTGGATCATGCCAGACAATATTTTCCTCACAGCCCCATA
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cDNA_rat	7351	CttTGGAAGCAGAGTCACGGTCCATCCAAATGGAACCTTGGAgatgagga
genomic_hu	890	CtaTGGAAGCAGAATCACAGTCCATAAAAATGGAACCTTGGAaattagga
cDNA_rat	7401	acatccGGCTTTCTGACTCTGCGGACTTCACCTGTGTGGttcggagcgag
genomic_hu	940	atgtgaGGCTTTCAGATTCAGCCGACTTTATCTGTGTGGcccgaaatgaa
cDNA_rat	7451	ggaGGAGAGAGTGTGTTGGTAGTGCAGTTAGAAGTCCTAGAAATGCTGAG
genomic_hu	990	ggtGGAGAGAGCGTGTTGGTAGTACAGTTAGAAGTACTGGAAATGCTGAG
cDNA_rat	7501	AAGACCAACATTCAGAAACCCATTCAACGAAAAagtcatcgcccaagctg
genomic_hu	1040	AAGACCGACATTTAGAAATCCATTTAATGAAAAaatagttgcccagctgg
cDNA_rat	7551	gcaagcccgtAGCACTGAACTGCTCTGTGGATGGGAACCCCCCACCTGAA
genomic_hu	1090	gaaagtccacAGCATTGAATTGCTCTGTTGATGGTAACCCACCACCTGAA
cDNA_rat	7601	attacCTGGATCTTACCTGACGGCACACAGTTTGCTAACAGACCAcacaa
genomic_hu	1140	ataatCTGGATTTTACCAAATGGCACACGATTTTCCAATGGACCAcaaag
cDNA_rat	7651	ttccccGTATCTGATGGCAGGCAATGGCTCTCTCATCCTTTACAAAgcaa
genomic_hu	1190	ttatcaGTATCTGATAGCAAGCAATGGTTCTTTTATCATTTCTAAAacaa
cDNA_rat	7701	ctcggaacaagtCAGGGAAGTATCGCTGTGCAGCCAGGAATAAGGTTGGC
genomic_hu	1240	ctcgggaggatgCAGGAAAATATCGCTGTGCAGCTAGGAATAAAGTTGGC
cDNA_rat	7751	TAcatcgagaaactcatcctgttagagATTGGGCAGAAGCCAGTCATTCT
genomic_hu	1290	TAtattgagaaattagtcatattagaaATTGGCCAGAAGCCAGTTATTCT
cDNA_rat	7801	GACATACGAACCAGGGAtggtgaagagcgTCAGTGGGGAACCGTTATCAC
genomic_hu	1340	TACCTATGCACCAGGGAcagtaaaaggcaTCAGTGGAGAATCTCTATCAC
cDNA_rat	7851	TGCATTGTGTGTCTGATGGgATCCCCAAGCCAAATGTCAAGTGGACTACA
genomic_hu	1390	TGCATTGTGTGTCTGATGGaATCCCTAAGCCAAATATCAAATGGACTATG
cDNA_rat	7901	CCGGGTGGccATGTAATCGACAGGCCTCAAGTGGATGGAAAATACATAcT
genomic_hu	1440	CCAAGTGGttATGTAGTAGACAGGCCTCAAATTAATGGGAAATACATAtT
cDNA_rat	7951	GCATGAAAATGGCACGCTGGTCATCAAAGCAACAACAGCtcacgaccaAG
genomic_hu	1490	GCATGACAATGGCACCTTAGTCATTAAAGAAGCAACAGCttatgacagAG
cDNA_rat	8001	GAAATTATATCTGTAGGGCTCAAAACAGTGTTGGCCAggcagttattagc
genomic_hu	1540	GAAACTATATCTGTAAGGCTCAAAATAGTGTTGGTCAtacactgattact
cDNA_rat	8051	gtgtCAGTGATGGTTGTGGCCTACCCTCCCCGAATCATAAActacctACC
genomic_hu	1590	gttcCAGTAATGATTGTAGCCTACCCTCCCCGAATTACAAAtcgtccACC
cDNA_rat	8101	CAGGAACATGCTCAGGAGGACAGGGGAAGCCatgCAGCTCCACTGTGTGG
genomic_hu	1640	CAGGAGTATTGTCACCAGGACAGGGGCAGCCtttCAGCTCCACTGTGTGG
cDNA_rat	8151	CCTTGGGAATCCCCAAGCCAaAAGTCACCTGGGAGACGCCAAGACACTCC
genomic_hu	1690	CCTTGGGAGTTCCCAAGCCAgAAATCACATGGGAGATGCCTGACCACTCC
cDNA_rat	8201	CTGCTCTCAAaagcaacagcaagaaaacccCATAGAAGTGAGATGCTTCA
genomic_hu	1740	CTTCTCTCAAcggcaagtaaagagaggacaCATGGAAGTGAGCAGCTTCA
cDNA_rat	8251	CCCACAAGGTACGCTgGTCATTCAGAATCTCCAAACCTCGGATTCCGGag
genomic_hu	1790	CTTACAAGGTACCCTaGTCATTCAGAATCCCCAAACCTCCGATTCTGGga
cDNA_rat	8301	tcTATAAGTGCAGAGCTCAGAACCTACTTGGgacTGATTACGCAACAACT
genomic_hu	1840	taTACAAATGCACAGCAAAGAACCCACTTGGtagTGATTATGCAGCAACG
cDNA_rat	8351	TACATCCAGGTACTCTGACAGGAAgggggagactaaaattcaacagaagt
genomic_hu	1890	TATATTCAAGTAATCTGACATGAAataataaagtcaacaacatctgggca

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cDNA_rat      8401   ccacatccacagggTTTATTTTTTGGAAGAAGTTTAATCAAAGGCAGCCA
genomic_hu    1940   gaa----------TTTATTTTTTGGAAGAAGTTTAATCAAAGGCAGCCA

cDNA_rat      8451   TAGGCATGTAAATGAgtcTGAATACATTTACAGTATTAAATTTACAATGG
genomic_hu    1979   TAGGCATGTAAATGAattTGAATACATTTACAGTATTAAATTTACAATGA

cDNA_rat      8501   ACATGCgatga-----GACTTGTAAATGAAAGCATTGTGAACTGAaaccg
genomic_hu    2029   ACATGCaaaataaaagGACTTGTAAATAAATGCATTATGAACTGAtgata

cDNA_rat      8546   agtctctg-----TGGATCTCAAAGCAAACTCTTAACTTAAGGCACTTTg
genomic_hu    2079   ctgatttatttaaTGGATCTCAAAACAAACTTTTAACTTAAGGCACTTTt

cDNA_rat      8591   ATTTTGCCAACAAATAATAACAAACAttaagagaaaaaaatgatcCACTA
genomic_hu    2129   ATTTTGCCAACAAATAACAATAAACAaacattgaaacggtt----CACTA

cDNA_rat      8641   CGAAATAACAAACGGCTAATGCACCTGAATTctcagtaaaaagacctttc
genomic_hu    2175   TAAAATAACAAATGGCTAATGTACCTGAATTtttcagtaaaaaaatgaac

cDNA_rat      8691   tctcgctaacagttgCCAGCTGCCTCGTGTCTGTTTCCTACCAATGTCAC
genomic_hu    2225   ttctaata-------CCAGTTGCCTAGTGTCCACCTCCTATCAATGTTAC

cDNA_rat      8741   AAACAtcgcacacagggtGAATGGAGTCAACGGGAAAGATTAAGTTTGCG
genomic_hu    2268   AAGCAtggcactca----GAACAGAGACAATGGAAAATATTAAATCTGCA

cDNA_rat      8791   GTCtgtgtaaatctca------------ATGTACAAATATTCTGtcncTG
genomic_hu    2314   ATCtttatgatgtaaatttaccatcctgATGTATAAATATTTTG----TG
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exon1 (2342-2397)

```
cDNA_rat      8791   GTCtgtgtaaatctca------------ATGTACAAATATTCTGtcncTG
genomic_hu    2314   ATCtttatgatgtaaatttaccatcctgATGTATAAATATTTTG----TG

cDNA_rat      8829   GTTTATAAACATTTTGATAAAACCGAAAAAAAAAAAAAaaaaaaaaaaaa
genomic_hu    2360   GTTTATAAATTTTTTTGCTAAAACCTACAGAAAATAAGcactgaactgtc
```

(Genomic human OCP: SEQ ID NO:4)
(cDNA rat: SEQ ID NO:5)

Figure 11

Exon/Intron No.	Exon start	Exon end	Exon length	Intron length	Remarks
1	1	208	208	69	No valid splice site found upstream this exon
2	277	429	153	18	
3	447	485	39	1561	
4	2046	2244	199	1351	
5	3595	3724	130	3254	
6	6978	7359	382	4123	
7	11482	14903	3422	38	
8	14941	15307	367	51	
9	15358	15825	468	1039	
10	16864	~17760	~897	?	Last exon might be complete
11	?(1)	2317	~2317	25	Exon is not complete and start site is not known
12	2342	2397	56	-	

FIGURE 12

608 Human translated nucleotide sequence (ORF)

ATGAAGGTAAAAGGCAGAGGAATCACCTGCTTGCTGGTCTCCTTTGCTGT
GATCTGCCTGGTCGCCACCCCTGGGGGCAAGGCCTGTCCTCGCCGCTGTG
CCTGTTATATGCCTACGGAGGTACACTGCACATTTCGGTACCTGACTTCCA
TCCCAGACAGCATCCCGCCCAATGTGGAACGCATCAATTTAGGATACAAC
AGCTTGGTTAGATTGATGGAAACAGATTTTTCTGGCCTGACCAAACTGGA
GTTACTCATGCTTCACAGCAATGGCATTCACACAATCCCTGACAAGACCTT
CTCAGATTTGCAGGCCTTGCAGGTCTTAAAAATGAGCTATAATAAAGTCC
GAAAACTTCAGAAAGATACTTTTTATGGCCTCAGGAGCTTGACACGATTG
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CCACCCAGATACATTTGTCTCTTTGAGCTACCTCCAGATATTTAAAATCTC
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GTCTCAGCTGCAGCTTTCCAGTGTGCCAAGCCAACCATTGACTCATCCCTG
AAATCAAAGAGCCTGACTATTCTGGAAGACAGTAGTTCTGCTTTCATCTCT
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CAGTCTGGAAATGAAGCTAACATGGTCTGCAGTATTCAAAAGCCCTCAAG
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AAAATACCACAGTGAGCCCACCCCCAGTGGTCACCCAACTCCCAAACATA
CCTGGTGAAGAAGACGATTCCTCAGGCATGCTCGCTCTACATGAGGAATT

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CCAACAAACTATTATTAGAGTCAGTAAATACCACAAATAGTCATCAGACA
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TACTCAAATACTTAGCACCTCCACGTTCCCTTCAGATCCACACACAGCTGC
TCATTCTCAGTTTCCGATCCCTAGAAATAGTACAGTTAACATCCCGCTGTT
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CACTGTGTGGCCTTGGGAGTTCCCAAGCCAGAAATCACATGGGAGATGCC
TGACCACTCCCTTCTCTCAACGGCAAGTAAAGAGAGGACACATGGAAGTG
AGCAGCTTCACTTACAAGGTACCCTAGTCATTCAGAATCCCCAAACCTCC
GATTCTGGGATATACAAATGCACAGCAAAGAACCCACTTGGTAGTGATTA
TGCAGCAACGTATATTCAAGTAATCTGA

Figure 13

A

Region						
General	Rat	Human	Region Length	% identity	% positives	% gaps
1-655	1-655	1-653	655	76	86	0
656-726	656-726	654-724	71	46	62	0
727-779	727-779	725-777	53	77	86	0
780-1634	780-1617	778-1612	655	38	53	4
1635-end	1618-end	1613-end	980	74	85	0
	Total	Alignment	2614	62	74	1

B

Region					
Rat	Mouse	Length	% identity	% positives	% gaps
1-238	1-238	238	91	92	1

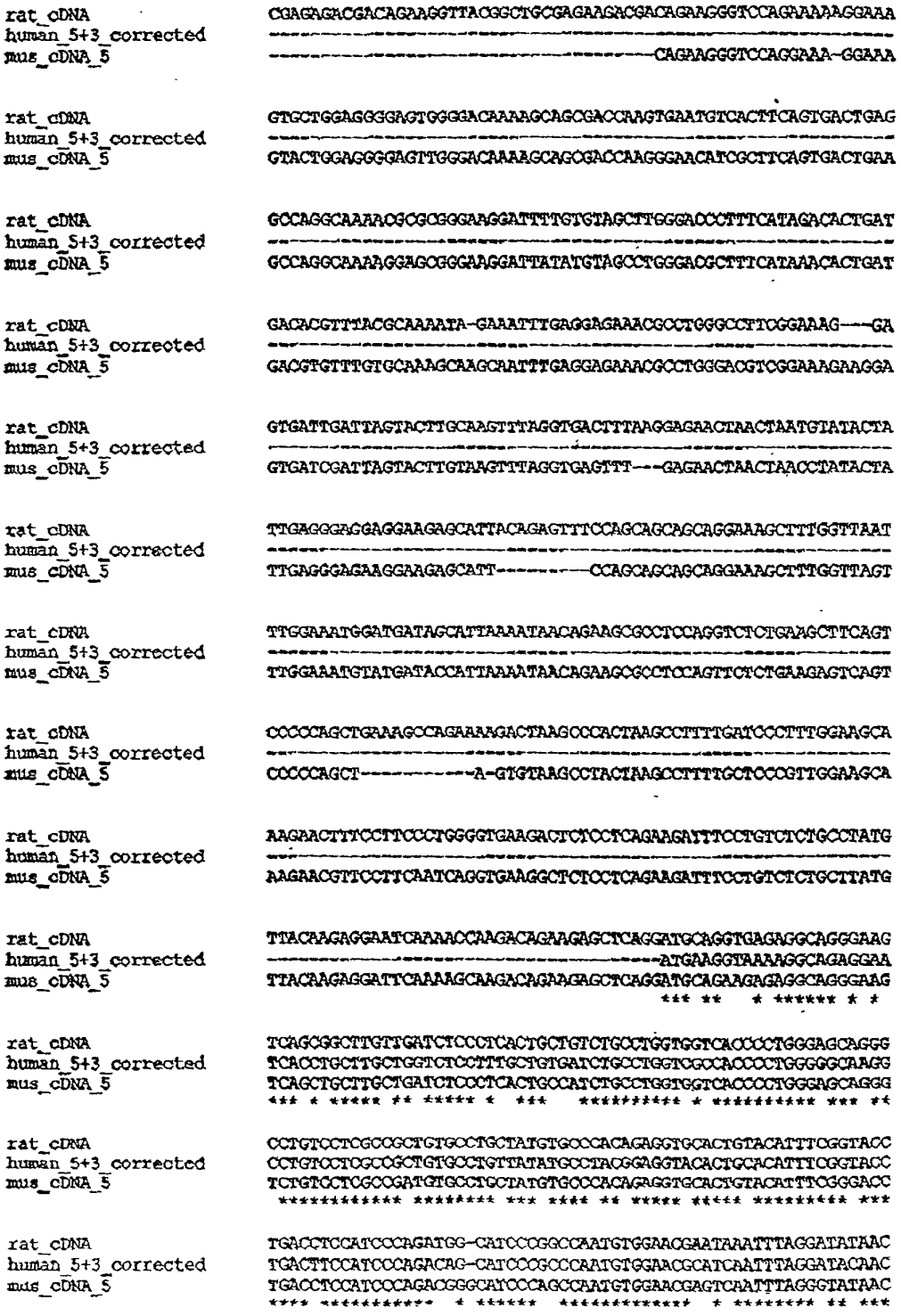
C

Region				
General	Rat	Human	Region Length	% identity
1-1965	1-1965	1-1965	1965	83
1966-2178	1966-2178	1966-2178	213	86
2179-2337	2179-2337	2179-2337	159	86
2338-4893	2338-4893	2338-4863	2565	63
4894-7833	4852-7791	4864-7761	2940	80
	Total	Alignment	7842	80

D

Region				
General	Rat	Mouse	Region Length	% identity
1-720	1-718	1-720	720	93

Figure 14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human_5+3_corrected
mus_cDNA_5
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TGACTTCCATCCCAGACAG-CATCCCGCCCAATGTGGAACGCATCAATTTAGGATACAAC
TGACCTCCATCCCAGACGGGCATCCCAGCCAATGTGGAACGAGTCAATTTAGGGTATAAC

```
rat_cDNA                AGCCTTACTAGATTGACAGAAAACGACTTTGATGGCCTGAGCAAACTGGAGTTACTCATG
human_5+3_corrected     AGCTTGGTTAGATTGATGGAAACAGATTTTTCTGGCCTGACCAAACTGGAGTTACTCATG
mus_cDNA_5              AGCCTCACTAGATTGACAGAAAATGACTTTTCTGGCCTGAGCAGACTGGAGTTACTCATG
                        *** *   ********  ****  ** ***  ******** ** ******************

rat_cDNA                CTGCACAGTAATGGCATTCACAGAGTCAGTGACAAGACCTTCTCGGGCTTGCAGTCCTTG
human_5+3_corrected     CTTCACAGCAATGGCATTCACACAATCCCTGACAAGACCTTCTCAGATTTGCAGGCCTTG
mus_cDNA_5              CTGCACAGCAATGGCATTCACAGAGTCAGTGACAAGACCTTCTCGGGCTTGCAGTCCTTG
                        ** ***** ************** * **  ***************  *  ******* *****

rat_cDNA                CAGGTCTTAAAAATGAGCTATAACAAAGTCCAAATCATTCGGAAGGATACTTTCTACGGA
human_5+3_corrected     CAGGTCTTAAAAATGAGCTATAATAAAGTCCGAAAACTTCAGAAAGATACTTTTTATGGC
mus_cDNA_5              CAGGTCTTAAAAATGAGCTATAACAAAGTCCAAATAATTGAGAAGGATACTTTGTATGGA
                        ************************ ******* **    **  *** ******** ** **

rat_cDNA                CTCGGGAGCTTGGTCCGGTTGCACCTGGATCACAACAACATTGAATTCATCAACCCTGAG
human_5+3_corrected     CTCAGGAGCTTGACACGATTGCACATGGACCACAACAATATTGAGTTTATAAACCCAGAG
mus_cDNA_5              CTCAGGAGCTTGACCCGGTTGCACCTGGATCACAACAACATTGAGTTTATCAACCCCGAG
                        *** ********    ** ****** **** ******** ***** ** ** ***** ***

rat_cDNA                GCCTTTTATGGACTTACCTCGCTCCGCTTGGTACATTTAGAAGGAAACCGGCTCACAAAG
human_5+3_corrected     GTTTTTTATGGGCTCAACTTTCTCCGCCTGGTGCACTTGGAAGGAAATCAGCTCACTAAG
mus_cDNA_5              GCGTTTTACGGACTCACCTTGCTCCGCTTGGTACATCTAGAAGGAAACCGGCTGACAAAG
                        *  ***** ** ** * **  ****** **** **  * ******** * *** ** ***

rat_cDNA                CTCCATCCAGACACATTTGTCTCATTAAGCTATCTCCAGATATTTAAAACCTCTTTCATT
human_5+3_corrected     CTCCACCCAGATACATTTGTCTCTTTGAGCTACCTCCAGATATTTAAAATCTCTTTCATT
mus_cDNA_5              CTCCATCCAGACACATTTGTCTCTTTGAGCTATCTCCAGATATTTAAAACCTCCTTCATT
                        ***** ***** ************ ** ****** ***************** *** ******

rat_cDNA                AAGTACCTGTTCTTGTCTGATAACTTCCT-GACCTCCCTCCCAAAAGAAATGGTCTCCTA
human_5+3_corrected     AAGTTCCTATACTTGTCTGATAACTTCCT-GACCTCCCTCCCTCAAGAGATGGTCTCCTA
mus_cDNA_5              AAGNACCTGTACTTGTATGATAACTTCATTGACCTCCCTCCCAAAAGAAATGGTCTCCTC
                        ***  *** * ***** ********** * ************  **** **********

rat_cDNA                CATGCCAAACCTAGAAAGCCTGTATTTGCATGGAAACCCATGGACCTGTGACTGCCATTT
human_5+3_corrected     TATGCCTGACCTAGACAGCCTTTACCTGCATGGAAACCCATGGACCTGTGATTGCCATTT
mus_cDNA_5              TATGCCAAACCTAGAAAGCCTTTACTTGCATGGAAACCCATGGACCTGTGACTGCCATTT
                         *****  ******* *****  **  ************************** ********

rat_cDNA                AAAGTGGTTGTCTGAGTGGATGCAGGGAAACCCAGATATAATAAAATGCAAGAAAGACAG
human_5+3_corrected     AAAGTGGTTGTCTGACTGGATACAGGNNNNNCCAGATGTAATAAAATGCAAAAAAGATAG
mus_cDNA_5              AAAGTGGTTGTCCGAGTGGATGCAGGGAAACCCAGGTA-ACTATCTTGT-----TTGTTTG
                        ************ ** ***** ****     **** *  * **   **       *  *

rat_cDNA                AAGCTCTTCCAGTCCTCAGCAATGTCCCCT-TTGCATGAACCCCAGGATCTCTAAAGGCA
human_5+3_corrected     AAGTCCCTCTAGTGCTCAGCAGTGTCCACT-TTGCATGAACCCTAGGACTTCTAAAGGCA
mus_cDNA_5              TTTCTTTTTTTATARKACGTATTTTCCTCAATTTCATTTAGAATGATATCCCAAAAGTC-
                              *    *      * * * *** *  ** ***  *       *   * **** *

rat_cDNA                GACCCTTTGCTATGGTACCATCTGGAGCTTTCCTATGTACAAAGCCAACCATTGATCCAT
human_5+3_corrected     AGCCGTTAGCTATGGTCTCAGCTGCAGCTTTCCAGTGTGCCAAGCCAACCATTGACTCAT
mus_cDNA_5              -CCCCATAACCTCCCCCCCA--------CTTCCCTACCTACCCATTC--CCATTTTTTGGC
                          **  *  *          **        *** **    * *  *  *  *****

rat_cDNA                CACTGAAGTCAAAGAGCCTGGTTACTCAGGAGGACAATGGATCTGCCTCCACCTCACCTC
human_5+3_corrected     CCCTGAAATCAAAGAGCCTGACTATTCTGGAAGACAGTAGTTCTGCTTTCATCTCTCCCC
mus_cDNA_5              CCTGGCATTCCCC----------------------------------------------
                        *   * * **

rat_cDNA                AAGATTTCATAGAACCCTTTGGCTCCTTGTCTTTGAACATGACANANNTNTCTGGAAATA
human_5+3_corrected     AAGGTTTCATGGCACCCTTTGGCTCCCTCACTTTGAATATGACAGATCAGTCTGGAAATG
mus_cDNA_5              ----------------------------------------------------------

rat_cDNA                AGGCCGACATGGTCTGTAGTATCCAAAAGCCATCAAGGACATCACCAACTGCATTCACTG
human_5+3_corrected     AAGCTAACATGGTCTGCAGTATTCAAAAGCCCTCAAGGACATCACCCATTGCATTCACTG
mus_cDNA_5              ----------------------------------------------------------
```


rat_cDNA AAGAAAATGACTACATCATGCTAAATGCGTCATTTTCCACAAATCTTGTGTGCAGTGTAG
human_5+3_corrected AAGAAAATGACTACATCGTGCTAAATACTTCATTTTCAACATTTTTGGTGTGCAACATAG
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human_5+3_corrected ATTACGGTCACATTCAGCCAGTGTGGCAAATTTTGGCTTTGTACAGTGATTCTCCTCTGA
mus_cDNA_5
rat_cDNA TACTAGAAAGGAAGCCCCAGCTTACCGAGACTCCTTCACTGTCTTCTAGATATAAACAGG
human_5+3_corrected TACTAGAAAGGAGCCACTTGCTTAGTGAAACACCGCAGCTCTATTACAAATATAAACAGG
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human_5+3_corrected CATTACAGATCCAGTACTCCAGTGATGCTCAAATCACTTTACCAAGAGCAGAGATGAGGC
mus_cDNA_5
rat_cDNA CGGAGAGACTCAAATGGACCATGATCCTGATGATGAACAATCCCAAACTGGAACGCACTG
human_5+3_corrected CAGTGAAACACAAATGGACTATGATTCAAGGGATAACAATACTAAGCTGGAACATACTG
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rat_cDNA TGGAATGGCTTCTAGCTGATGGGAGTAAAGTGAGAGCCCCTTACGTTAGCGAGGATGGGC
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mus_cDNA_5
rat_cDNA GAATCCTAATAGACAAAAATGGGAAGTTGGAACTGCAGATGGCTGACAGCTTTGATGCAG
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mus_cDNA_5
rat_cDNA GTCTTTACCACTGCATAAGCACCAATGATGCAGATGCGGATGTTCTCACATACAGGATAA
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mus_cDNA_5
rat_cDNA CTGTGGTAGAGCCCTATGGAGAAAGCACACATGACAGTGGAGTCCAGCACACAGTGGTTA
human_5+3_corrected CTGTGGTAGAACCTTTGGTCGAAGCCTATCAGGAAAATGGGATTCATCACACAGTTTTCA
mus_cDNA_5
rat_cDNA CGGGTGAGACGCTCGACCTTCCATGCCTTTCCACGGGTGTTCCAGATGCTTCTATTAGCT
human_5+3_corrected TTGGTGAAACACTTGATCTTCCATGCCATTCTACTGGTATCCCAGATGCCTCTATTAGCT
mus_cDNA_5
rat_cDNA GGATTCTTCCAGGGAACACTGTGTTCTCTCAGCCATCAAGAGACAGGCAAATTCTTAACA
human_5+3_corrected GGGTTATTCCAGGAAACAATGTGCTCTATCAGTCATCAAGAGACAAGAAAGTTCTAAACA
mus_cDNA_5

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rat_cDNA                ATGGGACCTTAAGAATATTACAGGTTACGCCAAAAGATCAAGGTCATTACCAATGTGTGG
human_5+3_corrected     ATGGCACATTAAGAATATTACAGGTCACCCCGAAAGACCAAGGTTATTATCGCTGTGTGG
mus_cDNA_5              ----------------------------------------------------------

rat_cDNA                CTGCCAACCCATCAGGGGCCGACTTTTCCAGTTTTAAAGTTTCAGTTCAAAAGAAAGGCC
human_5+3_corrected     CAGCCAACCCATCAGGGGTTGATTTTTTGATTTTCCAAGTTTCAGTCAAGATGAAAGGAC
mus_cDNA_5              ----------------------------------------------------------

rat_cDNA                AAAGGATGGTTGAGCATGACAGGGAGGCAGGTGGATCTGGACTTGGAGAACCCAACTCCA
human_5+3_corrected     AAAGGCCCTTGGAGCATGATGGAGAAACAGAGGGATCTGGACTTGATGAGTCCAATCCTA
mus_cDNA_5              ----------------------------------------------------------

rat_cDNA                GTGTTTCCCTTAAGCAGCCAGCATCTTTGAAACTCTCTGCATCAGCTTTGACAGGGTCAG
human_5+3_corrected     TTGCTCATCTTAAGGAGCCACCAGGTGCACAACTCCGTACATCTGCTCTGATGGAGGCTG
mus_cDNA_5              ----------------------------------------------------------

rat_cDNA                AGGCTGGAAAACAAGTCTCCGGTGTACATAGGAAGAACAAACATAGAGACTTAATACATC
human_5+3_corrected     AGGTTGGAAAACACACCTCAAGCACAAGTAAGAGGCACAACTATCGGGAATTAACACTCC
mus_cDNA_5              ----------------------------------------------------------

rat_cDNA                GGCGGCGTGGGGATTCCACGCTCCGGCGATTCAGGGAGCATAGGAGGCAGCTCCCTCTCT
human_5+3_corrected     AGCGACGTGGAGATTCAACACATCGACGTTTTAGGGAGAATAGGAGGCATTTCCCTCCCT
mus_cDNA_5              ----------------------------------------------------------

rat_cDNA                CTGCTCGGAGAATTGACCCGCAACGCTGGGCAGCACTTCTAGAAAAAGCCAAAAAGAATT
human_5+3_corrected     CTGCTAGGAGAATTGACCCACAACATTGGGCGGCACTGTTGGAGAAAGCTAAAAAGAATG
mus_cDNA_5              ----------------------------------------------------------

rat_cDNA                CTGTGCCAAAAAAGCAAGAAAATACCACAGTAAAGCCAGTGCCACTGGCTGTTCCCCTCG
human_5+3_corrected     CTATGCCAGACAAGCGAGAAAATACCACAGTGAGCCCACCCCCAGTGGTCACCCAACTCC
mus_cDNA_5              ----------------------------------------------------------

rat_cDNA                TGGAACTCACTGACGAGGAAAAGGATGCCTCTGGCATGATTCCTCCAGATGAAGAATTCA
human_5+3_corrected     CAAACATACCTGGTGAAGAAGACGATTCCTCAGGCATGCTCGCTCTACATGAGGAATTTA
mus_cDNA_5              ----------------------------------------------------------

rat_cDNA                TGGTTCTGAAAACTAAGGCTTCTGGTGTCCCAGGAAGGTCACCAACTGCTGACTCTGGAC
human_5+3_corrected     TGGTCCCGGCCACTAAAGCTTTGAACCTTCCAGCAAGGACAGTGACTGCTGACTCCAGAA
mus_cDNA_5              ----------------------------------------------------------

rat_cDNA                CAGTAAATCATGGTTTTATGACGAGTATAGCTTCTGGCACAGAAGTCTCAACTGTGAATC
human_5+3_corrected     CAATATCTGATAGTCCTATGACAAACATAAATTATGGCACAGAACTCTCCGTTGTGAATT
mus_cDNA_5              ----------------------------------------------------------

rat_cDNA                CACAAACACTACAATCTGAGCACCTTCCTGATTTCAAATTATTTAGTGTAACAAACGGTA
human_5+3_corrected     CACAAATACTACCACCTGAAGAACCCACAGATTTCAAACTGTCTACTGCTATTAAAACTA
mus_cDNA_5              ----------------------------------------------------------

rat_cDNA                CAGCTGTGACAAAGAGTATGAACCCATCCATAGCAAGCAAAATAGAAGATACAACCAACC
human_5+3_corrected     CAGCCATGTCAAAGAATATAAACCCAACCATGTCAAGCCAAATACAAGGCACAACCAATC
mus_cDNA_5              ----------------------------------------------------------

rat_cDNA                AAAACCCAATCATTATCTTTCCATC----------AGTAGCTGAAATTCGAGATTCTG-CT
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mus_cDNA_5              ----------------------------------------------------------
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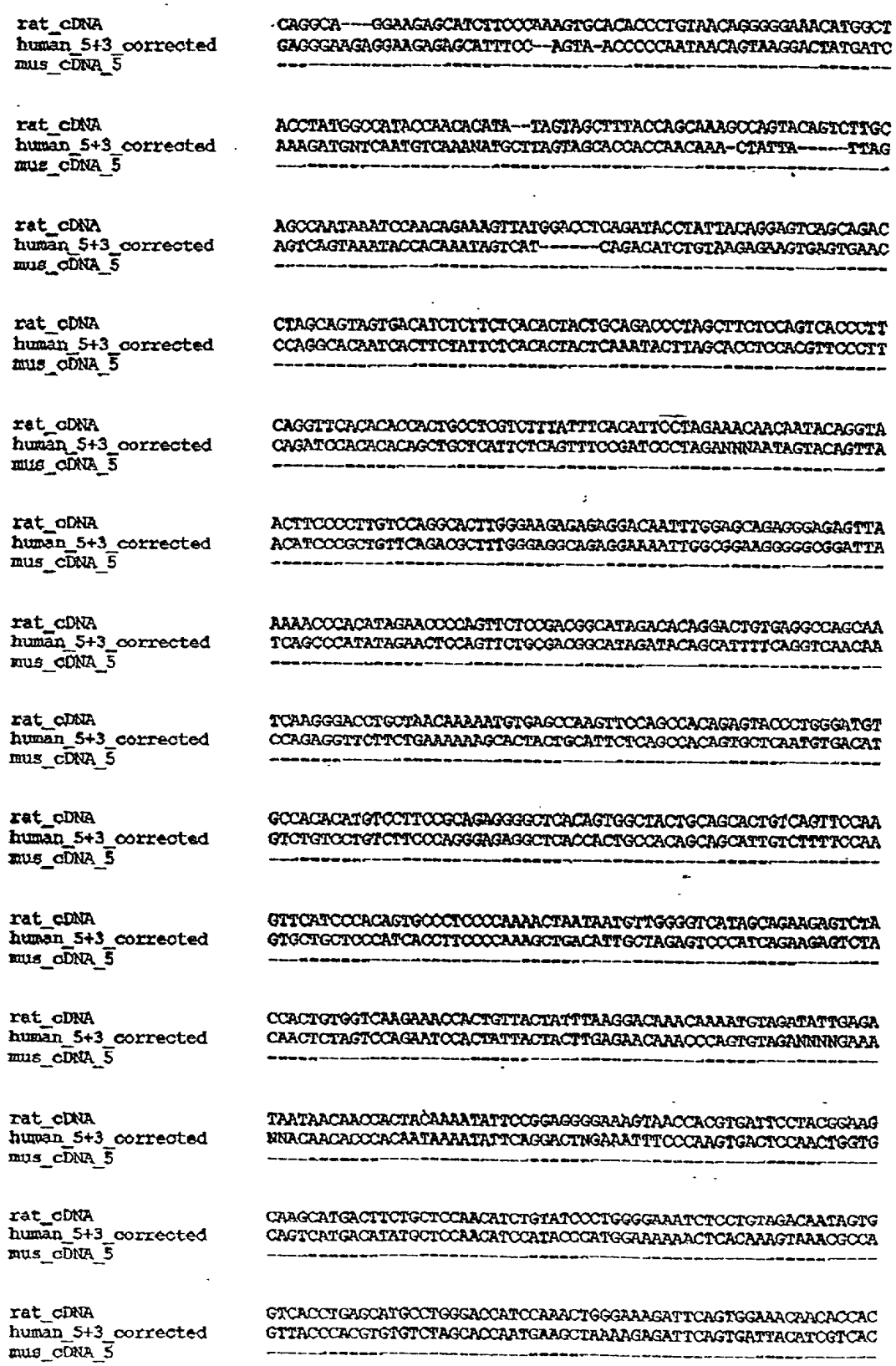
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rat_cDNA                TTCCCAGCCCCCTCAGCACACCCTCAATACCAA------CAAGCACAAAATTCTCAAAGA
human_5+3_corrected     TTTCAGGTGCTATCACCAAGCCACCAATGACTATTATAGCCATTACAAGGTTTTCAAGAA
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                GGAAAACTCCCTTGCACCAGATCTTTGTAAATAACCAGAAGAAGGAGGGGATGTTAAAGA
human_5+3_corrected     GGAAAATTCCCTGGCAACAGAACTTTGTAAATAACCATAACCCAAAAGGCAGATTAAGGA
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                ATCCATATCAATTCGGTTTACAAAAGAACCCAGCCGCAAAGCTTCCCAAAATAGCTCCTC
human_5+3_corrected     ATCAACATAAAGTTAGTTTACAAAAAAGCACAGCTGTGATGCTTCCTAAAACATCTCCTG
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TTTTACCCACAG-GTCAGAGTTCCCCCTCAGATTCTACAACTCTCTTGACAAGTCCGCCA
human_5+3_corrected     CTTTACC-ACAGAGACAAAGTTCCCCTTTCCATTTCACCACACTTTCAACAAGTGTGATG
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                CCAGCTCTGTCTACAACAATGGCTGCCACTCAGAACAAGGGCACTGAAGTAGTATCAGGT
human_5+3_corrected     CAAATTCCATCTAATACCTTGACTACCGCTCACCACACTACGACCAAA--ACACACAA-T
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                GCCAGAAGTCTCTCAGCAGGGAAGAAGCAGCCCTTCACCAACTCCTCTCCAG-TGCTTCC
human_5+3_corrected     CCTGGAAGTCTTCCAACAAAGAAGGAGCTTCCCTTC-CCACCCCTTAACCCTATGCTTCC
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TAGCACCATAAGCAAGAGATCTAATACATTAAACTTCTTGTCAACGGAAACCCCCACAGT
human_5+3_corrected     TAGTATTATAAGCAAAGACTCAAGTACAAAAAGCATCATATCAACGCAAACAGCAACCGC
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                GACAAGTCCTACTGCTACTGCATCTGTCATTATGTCTGAAACCCAACGAACAAGATCCAA
human_5+3_corrected     AACAACTCCTACCTTCCCTGCATCTGTCATCACTTATGAAACCCAAACAGAGAGATCTAG
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                AGAAGCAAAAGACCAAATAAAGGGGCCTCG---GAAGAACAGAAACAACGCAAACACCAC
human_5+3_corrected     AGCACAAACAATACAAAGAGAAGGACCTCAAAAGAAGAACAGGACTGACCCAAACATCTC
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                CCCCAGGCAGGTTTCTGGCTATAGTGCATACTCAGCTCTAACAACAGCTGATACCCCCTT
human_5+3_corrected     TCCAGACCAGAGTTCTGGCTTCACTACACCCACTGCTATGACNACCTCCTNNGCTCTNNN
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                GGCTTTCAGTCATTCCCCACGACAAGATGATGGTGGAAATGTAAGTGCAGTTGCTTATCA
human_5+3_corrected     NGCATTCACTCATTCCCCACCAGAAAACACAACTGGGATTTCAAGCACAATCAGTTTTCA
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                CTCAACAACCTCTCTTCTGGCCA---TAACTGAACTGTTTGAG-AAGTAC--ACCCAGAC
human_5+3_corrected     TTCAAGAACTCTTAATCTGACAGATGTGATTGAAGAACTAGCCCAAGCAAGTACTCAGAC
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TTTGGGAAATACAACAGCTTTGGAAACAACGTTGTTGAGCAAATCACAGGAGAGTACCAC
human_5+3_corrected     TTTGAAGAGCACAATTGCTTCTGAAACAACTTTGTCCAGCAAATCACACCAGAGTACCAC
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                AGTGAAAAGAGCCTCA---GACAC---ACCACCACCACTCCTCAGCAGTGGGGCGCCCCC
human_5+3_corrected     AACTAGGAAAGCATCATTAGACACTCAACCACCACCATTCTTGAGCAGCAGTGCTACTCT
mus_cDNA_5              ------------------------------------------------------------
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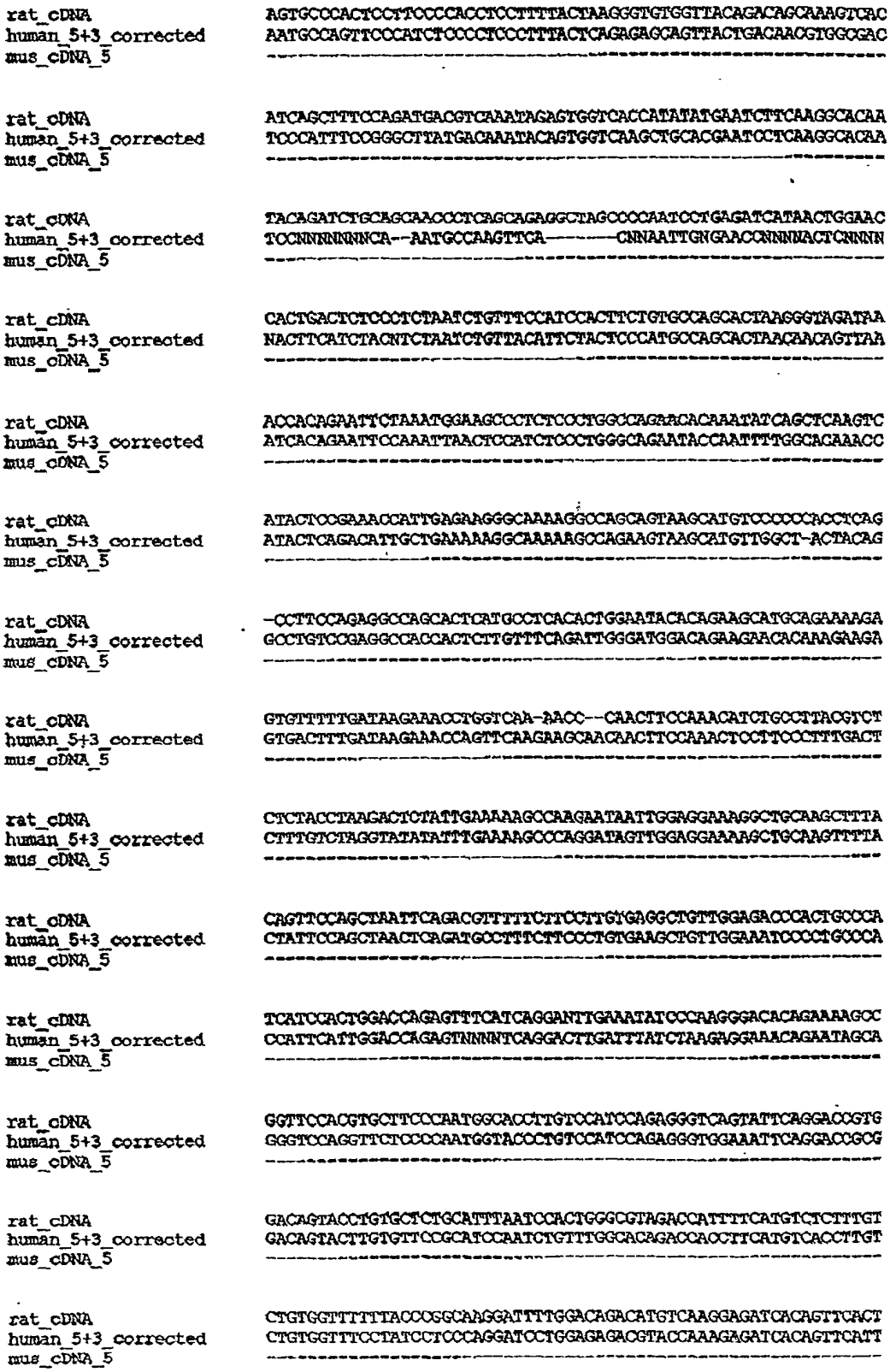
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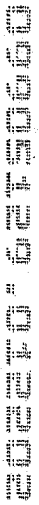

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rat_cDNA                TTGGAAGTACTGTGGAACTAAAGTGCAGAGTGGAGGGTATGCCGAGGCCTACGGTTTCCT
human_5+3_corrected     CCGGAAGCACTGTGGAACTGAAGTGCAGAGCAGAAGGTAGGCCAAGCCCTACAGTTACCT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                GGATACTTGCAAACCAAACGGTGGTCTCAGAAACGGCCAAGGGAAGCAGAAAGGTCTGGG
human_5+3_corrected     GGATTCTTGCAAACCAAACAGTTGTCTCAGAATCATCCCAGGGAAGTAGGCAGGCTGTGG
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TAACACCTGATGGAACATTGATCATCTATAATCTGAGTCTTTATGATCGTGGTTTTTACA
human_5+3_corrected     TGACGGTTGACGGAACATTGGTCCTCCACAATCTCAGTATTTATGACCGTGGCTTTTACA
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                AGTGTGTGGCCAGCAACCCATCTGGCCAGGATTCACTGTTGGTTAAGATACAAGTCATCA
human_5+3_corrected     AATGTGTGGCCAGCAACCCAGGTGGCCAGGATTCACTGCTGGTTAAAATACAAGTCATTG
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                CAGCTCCCCCTGTCATTATAGAGCAAAAGAGGCAAGCCATCGTTGGGGTTTTAGGTGGAA
human_5+3_corrected     CAGCACCACCTGTTATTCTAGAGCAAAGGAGGCAAGTCATTGTAGGCACTTGGGGTGAAA
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                GTTTGAAACTGCCCTGCACTGCAAAAGGAACTCCCCAGCCTAGTGTTCACTGGGTCCTTT
human_5+3_corrected     GTTTAAAACTGCCCTGTACTGCAAAAGGAACTCCTCAGCCCAGCGTTTACTGGGTCCTCT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                ATGATGGGACTGAACTAAAACCATTGCAGTTGACTCATTCCAGATTTTTCTTGTATCCAA
human_5+3_corrected     CTGATGGCACTGAAGTGAAACCATTACAGTTTACCAATTCCAAGTTGTTCTTATTTTCAA
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                ATGGAACTCTGTATATAAGAAGCATCGCTCCTTCAGTGAGGGGCACTTATGAGTGCATTG
human_5+3_corrected     ATGGGACTTTGTATATAAGAAACCTAGCCTCTTCAGACAGGGGCACTTATGAATGCATTG
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                CCACCAGCTCCTCAGGCTCAGAGAGAAGGGTAGTGATTCTTACTGTGGAAGAGGGAGAGA
human_5+3_corrected     CTACCAGTTCCACTGGTTCGGAGCGAAGAGTAGTAATGCTTACAATGGAAGAGCGAGTGA
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                CAATCCCCAGGATAGAAACTGCCTCTCAGAAATGGACTGAGGTGAATTTGGGTGAGAAAT
human_5+3_corrected     CCAGCCCCAGGATAGAAGCTGCATCCCAGAAAAGGACTGAAGTGAATTTTGGGGAGAAAT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TACTACTGAACTGCTCAGCTACTGGGGATCCAAAGCCTAGAATAATCTGGAGGCTGCCAT
human_5+3_corrected     TACTACTGAACTGCTCAGCCACTGGGGAGCCCAAACCCCAAATAATGTGGAGGTTACCAT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                CCAAGGCTGTCATCGACCAGTGGCACAGAATGGGCAGCCGAATCCACGTCTACCCAAATG
human_5+3_corrected     CCAAGGCTGTGGTCGACCAGTGG----------GCAGCTGGATCCACGTCTACCCTAATG
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                GATCCTTGGTGGTTGGGTCAGTGACGGAAAAAGACGCTGGTGACTACTTATGTGTGGCAA
human_5+3_corrected     GATCCCTGTTTATTGGATCAGTAACAGAAAAAGACAGTGGTGTCTACTTGTGTGTGGCAA
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                GAAACAAAATGGGAGATGACCTAGTCCTGATGCATGTCCGCCTGAGATTGACACCTGCCA
human_5+3_corrected     GAAACAAAATGGGGGATGATCTGATACTGATGCATGTTAGCCTAAGACTGAAACCTGCCA
mus_cDNA_5              ------------------------------------------------------------
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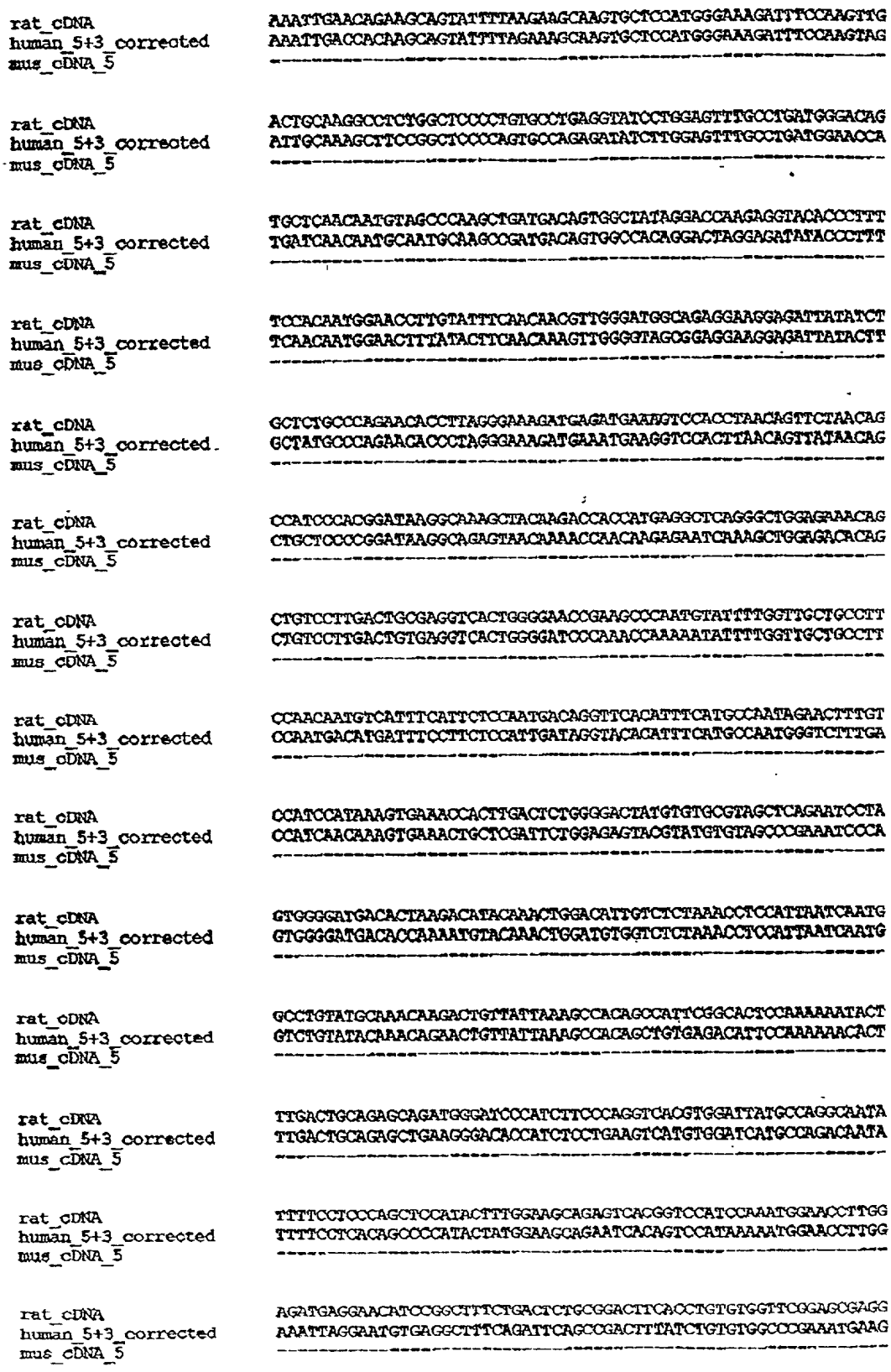
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human_5+3_corrected
mus_cDNA_5
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rat_cDNA                GAGGAGAGAGTGTGTTGGTAGTGCAGTTAGAAGTCCTAGAAATGCTGAGAAGACCAACAT
human_5+3_corrected     GTGGAGAGAGCGTGTTGGTAGTACAGTTAGAAGTACTGGAAATGCTGAGAAGACCGACAT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TCAGAAACCCATTCAACGAAAAAGTCATCGCCCAAGCTGGCAAGCCCGTAGCACTGAACT
human_5+3_corrected     TTAGAAATCCATTTAATGAAAAAATAGTTGCCCAGCTGGGAAAGTCCACAGCATTGAATT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                GCTCTGTGGATGGGAACCCCCCACCTGAAATTACCTGGATCTTACCTGACGGCACACAGT
human_5+3_corrected     GCTCTGTTGATGGTAACCCACCACCTGAAATAATCTGGATTTTACCAAATGGCACACGAT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TTGCTAACAGACCACACAATTCCCCGTATCTGATGGCAGGCAATGGCTCTCTCATCCTTT
human_5+3_corrected     TTTCCAATGGACCACAAAGTTATCAGTATCTGATAGCAAGCAATGGTTCTTTTATCATTT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                ACAAAGCAACTCGGAACAAGTCAGGGAAGTATCGCTGTGCAGCCAGGAATAAGGTTGGCT
human_5+3_corrected     CTAAAACAACTCGGGAGGATGCAGGAAAATATCGCTGTGCAGCTAGGAATAAAGTTGGCT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                ACATCGAGAAACTCATCCTGTTAGAGATTGGGCAGAAGCCAGTCATTCTGACATACGAAC
human_5+3_corrected     ATATTGAGAAATTAGTCATATTAGAAATTGGCCAGAAGCCAGTTATTCTTACCTATGCAC
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                CAGGGATGGTGAAGAGCGTCAGTGGGGAACCGTTATCACTGCATTGTGTGTCTGATGGGA
human_5+3_corrected     CAGGGACAGTAAAAGGCATCAGTGGAGAATCTCTATCACTGCATTGTGTGTCTGATGGAA
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TCCCCAAGCCAAATGTCAAGTGGACTACACCGGGTGGCCATGTAATCGACAGGCCTCAAG
human_5+3_corrected     TCCCTAAGCCAAATATCAAATGGACTATGCCAAGTGGTTATGTAGTAGACAGGCCTCAAA
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TGGATGGAAAATACATACTGCATGAAAATGGCACGCTGGTCATCAAAGCAACAACAGCTC
human_5+3_corrected     TTAATGGGAAATACATATTGCATGACAATGGCACCTTAGTCATTAAAGAAGCAACAGCTT
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                ACGACCAAGGAAATTATATCTGTAGGGCTCAAAACAGTGTTGGCCAGGCAGTTATTAGCG
human_5+3_corrected     ATGACAGAGGAAACTATATCTGTAAGGCTCAAAATAGTGTTGGTCATACACTGATTACTG
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TGTCAGTGATGGTTGTGGCCTACCCTCCCCGAATCATAAACTACCTACCCAGGAACATGC
human_5+3_corrected     TTCCAGTAATGATTGTAGCCTACCCTCCCCGAATTACAAATCGTCCACCCAGGAGTATTG
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                TCAGGAGGACAGGGGAAGCCATGCAGCTCCACTGTGTGGCCTTGGGAATCCCCAAGCCAA
human_5+3_corrected     TCACCAGGACAGGGGCAGCCTTTCAGCTCCACTGTGTGGCCTTGGGAGTTCCCAAGCCAG
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                AAGTCACCTGGGAGACGCCAAGACACTCCCTGCTCTCAAAAGCAACAGCAAGAAAACCCC
human_5+3_corrected     AAATCACATGGGAGATGCCTGACCACTCCCTTCTCTCAACGGCAAGTAAAGAGAGGACAC
mus_cDNA_5              ------------------------------------------------------------

rat_cDNA                ATAGAAGTGAGATGCTTCACCCACAAGGTACGCTGGTCATTCAGAATCTCCAAACCTCGG
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mus_cDNA_5              ------------------------------------------------------------
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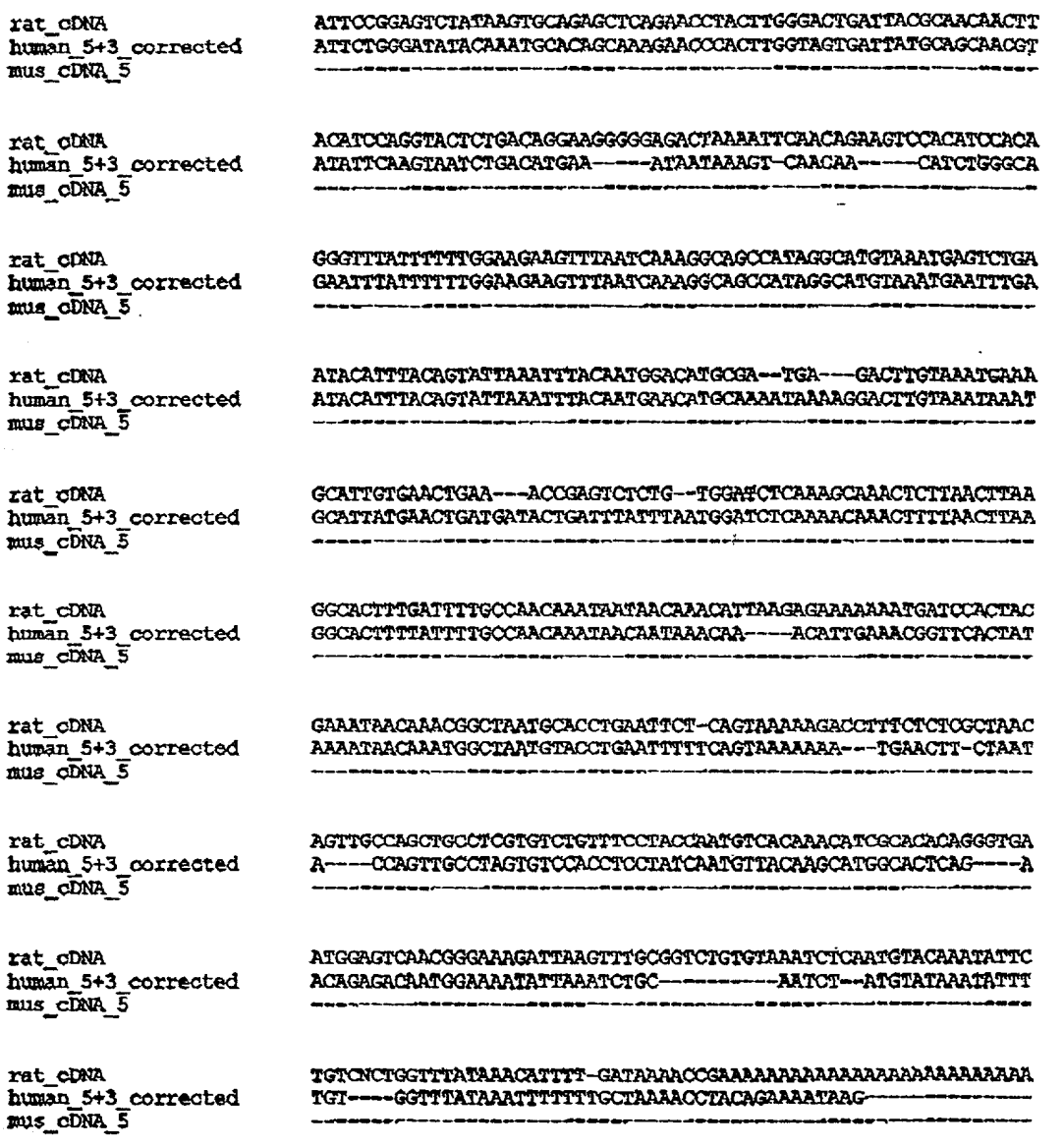

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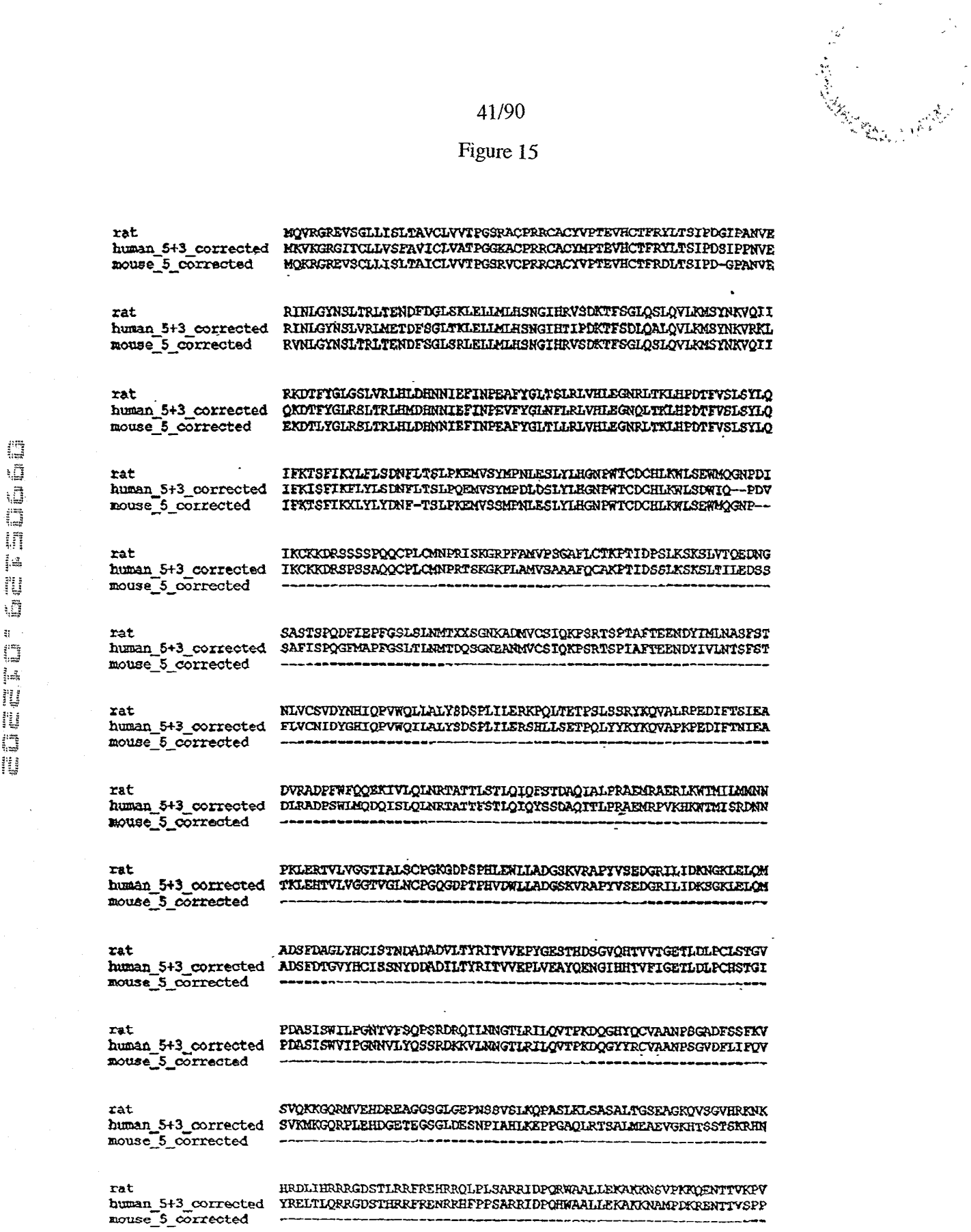
Figure 15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mouse_5_corrected MQKRGREVSCLLISLTAICLVVTPGSRVCPRRCACYVPTEVHCTFRDLTSIPD-GPANVE
rat RINLGYNSLTRLTENDFDGLSKLELLMLHSNGIHRVSDKTFSGLQSLQVLKMSYNKVQII
human_5+3_corrected RINLGYNSLVRLMETDFSGLTKLELLMLHSNGIHTIPDKTFSDLQALQVLKMSYNKVRKL
mouse_5_corrected RVNLGYNSLTRLTENDFSGLSRLELLMLHSNGIHRVSDKTFSGLQSLQVLKMSYNKVQII
rat RKDTFYGLGSLVRLHLDHNNIEFINPEAFYGLTSLRLVHLEGNRLTKLHPDTFVSLSYLQ
human_5+3_corrected QKDTFYGLRSLTRLHMDHNNIEFINPEVFYGLNFLRLVHLEGNQLTKLHPDTFVSLSYLQ
mouse_5_corrected EKDTLYGLRSLTRLHLDHNNIEFINPEAFYGLTLLRLVHLEGNRLTKLHPDTFVSLSYLQ
rat IFKTSFIKYLFLSDNFLTSLPKEMVSYMPNLESLYLHGNPWTCDCHLKWLSEWMQGNPDI
human_5+3_corrected IFKISFIKFLYLSDNFLTSLPQEMVSYMPDLDSLYLHGNPWTCDCHLKWLSDWIQ--PDV
mouse_5_corrected IFKTSFIKXLYLYDNF-TSLPKEMVSSMPNLESLYLHGNPWTCDCHLKWLSEWMQGNP--
rat IKCKKDRSSSSPQQCPLCMNPRISKGRPFAMVPSGAFLCTKPTIDPSLKSKSLVTQEDNG
human_5+3_corrected IKCKKDRSPSSAQQCPLCMNPRTSKGKPLAMVSAAAFQCAKPTIDSSLKSKSLTILEDSS
mouse_5_corrected ----------
rat SASTSPQDFIEPFGSLSLNMTXXSGNKADMVCSIQKPSRTSPTAFTEENDYIMLNASFST
human_5+3_corrected SAFISPQGFMAPFGSLTLNMTDQSGNEANMVCSIQKPSRTSPIAFTEENDYIVLNTSFST
mouse_5_corrected ----------
rat NLVCSVDYNHIQPVWQLLALYSDSPLILERKPQLTETPSLSSRYKQVALRPEDIFTSIEA
human_5+3_corrected FLVCNIDYGHIQPVWQILALYSDSPLILERSHLLSETPQLYYKYKQVAPKPEDIFTNIEA
mouse_5_corrected ----------
rat DVRADPFWFQQEKIVLQLNRTATTLSTLQIQFSTDAQIALPRAEMRAERLKWTMILMMNN
human_5+3_corrected DLRADPSWLMQDQISLQLNRTATTFSTLQIQYSSDAQITLPRAEMRPVKHKWTMISRDNN
mouse_5_corrected ----------
rat PKLERTVLVGGTIALSCPGKGDPSPHLEWLLADGSKVRAPYVSEDGRILIDKNGKLELQM
human_5+3_corrected TKLEHTVLVGGTVGLNCPGQGDPTPHVDWLLADGSKVRAPYVSEDGRILIDKSGKLELQM
mouse_5_corrected ----------
rat ADSFDAGLYHCISTNDADADVLTYRITVVEPYGESTHDSGVQHTVVTGETLDLPCLSTGV
human_5+3_corrected ADSFDTGVYHCISSNYDDADILTYRITVVEPLVEAYQENGIHHTVFIGETLDLPCHSTGI
mouse_5_corrected ----------
rat PDASISWILPGNTVFSQPSRDRQILNNGTLRILQVTPKDQGHYQCVAANPSGADFSSFKV
human_5+3_corrected PDASISWVIPGNNVLYQSSRDKKVLNNGTLRILQVTPKDQGYYRCVAANPSGVDFLIFQV
mouse_5_corrected ----------
rat SVQKKGQRMVEHDREAGGSGLGEPNSSVSLKQPASLKLSASALTGSEAGKQVSGVHRKNK
human_5+3_corrected SVKMKGQRPLEHDGETEGSGLDESNPIAHLKEPPGAQLRTSALMEAEVGKHTSSTSKRHN
mouse_5_corrected ----------
rat HRDLIHRRRGDSTLRRFREHRRQLPLSARRIDPQRWAALLEKAKKNSVPKKQENTTVKPV
human_5+3_corrected YRELTLQRRGDSTHRRFRENRRHFPPSARRIDPQHWAALLEKAKKNAMPDKRENTTVSPP
mouse_5_corrected ----------

```
rat                   PLAVPLVELTDEEKDASGMIPPDEEPMVLKTKASGVPGRSPTADSGPVNHGPMTSIASGT
human_5+3_corrected   PVVTQLPNIPGEEDDSSGMLALHEEPMVPATKALNLPARTVTADSRTISDSPMTNINYGT
mouse_5_corrected     ------------------------------------------------------------

rat                   EVS-TVNPQTLQSEHLPDFKLFSVTNGTAVTKSMNPSIASKIEDTTNQNPIIIPP----SV
human_5+3_corrected   EFSPVVNSQILPPEEPTDFKLSTAIKTTAMSKNINPTMSSQIQGTTNQHSSTVFPLLLGA
mouse_5_corrected     ------------------------------------------------------------

rat                   AEIRDSAQAGRAS--SQSAHPVTGGNMATYGHTNTYSSFTSKASTVLQPINPTKSYGPQI
human_5+3_corrected   TEFQDSDQMGRGREHFQSRPPITVRTMIKDVNVKMLSSTTNKL--LLESVNTTNSH--QT
mouse_5_corrected     ------------------------------------------------------------

rat                   PITGVSRPSSSDISSHTTADPSFSSHPSGSHTTASSLPHIPRNNNTGNFPLSRHLGRERT
human_5+3_corrected   SVREVSEPRHNHFYSHTTQILSTSTFPSDPHTAAHSQFPIPRNS-TVNIPLFRRFGRQRK
mouse_5_corrected     ------------------------------------------------------------

rat                   IWSRGRVENPHRTPVLRRHRHRTVRPAIKGPANKNVSQVPATEYPGMCHTCPSAEGLTVA
human_5+3_corrected   IGGRGRIISPYRTPVLRRHRYSIFRSTTRGSSEKSTTAFSATVLNVTCLSCLPRERLTTA
mouse_5_corrected     ------------------------------------------------------------

rat                   TAALSVPSSSHSALPKTNNVGVIAEESTTVVKKPLLLFKDKQNVDIEIITTTTTKYSGGES
human_5+3_corrected   TAALSFPSAAPITFPKADIARVPSEESTTLVQNPLLLLENKP--SVEKTTPTIKYFRTEI
mouse_5_corrected     ------------------------------------------------------------

rat                   NHVIPTEASMTSAPTSVSLGKSPVDNSGHLSMPGTIQTGKDSVETTPLPSPLSTP--SIP
human_5+3_corrected   SQVTPTGAVMTYAPTSIPMEKTHKVNASYPRVSSTNEAKRDSVITSSLSGAITKPPMTII
mouse_5_corrected     ------------------------------------------------------------

rat                   TSTKFSKRKTPLHQIFVNWQKEGMLKNPYQFGLQKNPAAKLPKIAPLLPTGQSSPSDST
human_5+3_corrected   AITRFSRRKIPWQQNFVNNHNPKGRLRNQHKVSLQKSTAVMLPKTSPALPQRQSSPFHFT
mouse_5_corrected     ------------------------------------------------------------

rat                   TLLTSPPPALSTTMAATQNKGTEVVSGARSLSAGKKQ-PFTNSSPVLPSTISKRSNTLNF
human_5+3_corrected   TISTSVMQIPSNTLTTAHHTTTKTHNPG-SLPT-KKELPFPPLNPMLPSIISKDSSTKSI
mouse_5_corrected     ------------------------------------------------------------

rat                   LSTETPT-VTSPTATASVIMSETQRTRSKEAKDQIKG-P-RKNRNNANTTPRQVSGYSAY
human_5+3_corrected   ISTQTAIPATTPTFPASVITYETQTERSRAQTIQREQEPQKKNRTDPNISPDQSSGFTTP
mouse_5_corrected     ------------------------------------------------------------

rat                   SALTTADTPLAFSHSPRQDDGGNVSAVAYHSTTS--LLAITELFEKYTQTLGNTTALETT
human_5+3_corrected   TAMTP---PALAFTHSPPENTTGISSTISFHSRTLNLTDVIEELAQASTQTLKSTIASETT
mouse_5_corrected     ------------------------------------------------------------

rat                   LLSKSQESTTVKRAS-DTP-PFLLSSGAPPVPTPSPPPFTKGVVTDSKVTSAFQMTSNRV
human_5+3_corrected   LSSKSHQSTTTRKASLDTPIPPFLSSSATIMPVPISPPFTQRAVTDTRGDSHFRLMTNTV
mouse_5_corrected     ------------------------------------------------------------

rat                   VTIYESSRHNTDLQQPSAEASPNPEIITGTTDSPSNLFPSTSVPALRVDKPQNSKWKPSP
human_5+3_corrected   VKLHESSRHN--LQMPSSQLEP--------LTSSTSNLLHSTPMPALTTVKSQNSKLTPSP
mouse_5_corrected     ------------------------------------------------------------

rat                   WPEHKYQLKSYSETIEKGKRPAVSMSPHLSLPEASTHASHWNTQKHAEKSVFDKKPGQNP
human_5+3_corrected   WAEYQFWHKPYSDIAEKGKKPEVSMLATTGLSEATTLVSDWDGQKNTKKSDFDKKPVQEA
mouse_5_corrected     ------------------------------------------------------------
```

```
rat                     -TSKHLPYVSLPKTLLKKPRIIGGKAASFTVPANSDVFLPCEAVGDPLPIIHWTRVSSGX
human_5+3_corrected     TTSKLLPFDSLSRYIFEKPRIVGGKAASFTIPANSDAFLPCEAVGNPLPTIHWTRVS-GL
mouse_5_corrected       ------------------------------------------------------------

rat                     EISQGTQKSRFHVLPNGTLSIQRVSIQDRGQYLCSAFNPLGVDHFHVSLSVVFYPARILD
human_5+3_corrected     DLSRGNQNSRVQVLPNGTLSIQRVEIQDRGQYLCSASNLFGTDHLHVTLSVVSYPPRILE
mouse_5_corrected       ------------------------------------------------------------

rat                     RHVKEITVHPGSTVELKCRVEGMPRPTVSWILANQTVVSETAKGSRKVWVTPDGTLIIYN
human_5+3_corrected     RRTKEITVHSGSTVELKCRAEGRPSPTVTWILANQTVVSESSQGSRQAVVTVDGTLVLHN
mouse_5_corrected       ------------------------------------------------------------

rat                     LSLYDRGFYKCVASNPSGQDSLLVKIQVIYAPPVIIEQKRQAIVGVLGGSLKLPCTAKGT
human_5+3_corrected     LSIYDRGFYKCVASNPGGQDSLLVKIQVIAAPPVILEQRRQVIVGTWGESLKLPCTAKGT
mouse_5_corrected       ------------------------------------------------------------

rat                     PQPSVHWVLYDGTELKPLQLTHSRFFLYPMGTLYIRSIAPSVRGIYSCIATSSSGSERRV
human_5+3_corrected     PQPSVYWVLSDGTEVKPLQFTNSKLFLFSNGTLYIRNLASSDRGTYECIATSSTGSERRV
mouse_5_corrected       ------------------------------------------------------------

rat                     VILTVEEGETIPRIETASQKWTEVNLGEKLLLNCSATGDPKPRIIWRLPSKAVIDQWHRM
human_5+3_corrected     VMLTMEERVTSPRIEAASQKRTEVNFGDKLLLNCSATGEPKPQIMWRLPSKAVVDQ-----
mouse_5_corrected       ------------------------------------------------------------

rat                     GSRIHVYPNGSLVVGSVTEKDAGDYLCVARNKMGDDLVLMHVRLRLTPAKIEQKQYFKKQ
human_5+3_corrected     GSWIHVYPNGSLFIGSVTEKDSGVYLCVARNKMGDDLILMHVSLRLKPAKIDHKQYFRKQ
mouse_5_corrected       ------------------------------------------------------------

rat                     VLHGKDFQVDCKASGSPVPEVSWSLPDGTVLNNVAQADDSGYRTKRYTLFHNGTLYFNNV
human_5+3_corrected     VLHGKDFQVDCKASGSPVPEISWSLPDGTNINNAMQADDSGHRTRRYTLFNNGTLYFNKV
mouse_5_corrected       ------------------------------------------------------------

rat                     GMAEEGDYICSAQNTLGKDEMKVHLTVLTAIPRIRQSYKTTMRLRAGETAVLDCEVTGEP
human_5+3_corrected     GVAEEGDYTCYAQNTLGKDEMKVHLTVITAAPRIRQSNKTNKRIKAGDTAVLDCEVTGDP
mouse_5_corrected       ------------------------------------------------------------

rat                     KPNVFWLLPSNNVISFSNDRFTFHANRTLSIHKVKPLDSGDYVCVAQNPSGDDTKTYKLD
human_5+3_corrected     KPKIFWLLPSNDMISFSIDRYTFHANGSLTINKVKLLDSGEYVCVARNPSGDDTKMYKLD
mouse_5_corrected       ------------------------------------------------------------

rat                     IVSKPPLINGLYANKTVIKATAIRHSKKYFDCRADGIPSSQVTWIMPGNIFLPAPYFGSR
human_5+3_corrected     VVSKPPLINGLYTNRTVIKATAVRHSKKHFDCRAEGTPSPEVMWIMPDNIFLTAPYYGSR
mouse_5_corrected       ------------------------------------------------------------

rat                     VTVHPNGTLEMRNIRLSDSADFTCVVRSEGGESVLVVQLEVLEMLRRPTFRNPFNEKVIA
human_5+3_corrected     ITVHKNGTLEIRNVRLSDSADFICVARNEGGESVLVVQLEVLEMLRRPTFRNPFNEKIVA
mouse_5_corrected       ------------------------------------------------------------

rat                     QAGKPVALNCSVDGNPPPEITWILPDGTQFANRPHNSPYIMAGNGSLILYKATRNKSGKY
human_5+3_corrected     QLGKSTALNCSVDGNPPPEIIWILPNGTRFSNGPQSYQYLIASNGSFIISKTTREDAGKY
mouse_5_corrected       ------------------------------------------------------------

rat                     RCAARNKVGYIEKLILLEIGQKPVILTYEPGMVKSVSGEPLSLHCVSDGIPKPNVKWTTP
human_5+3_corrected     RCAARNKVGYIEKLVILEIGQKPVILTYAPGTVKGISGESLSLHCVSDGIPKPNIKWTMP
mouse_5_corrected       ------------------------------------------------------------
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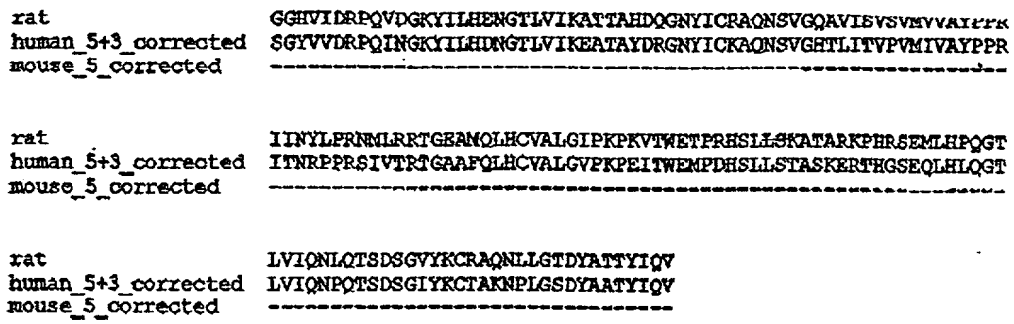
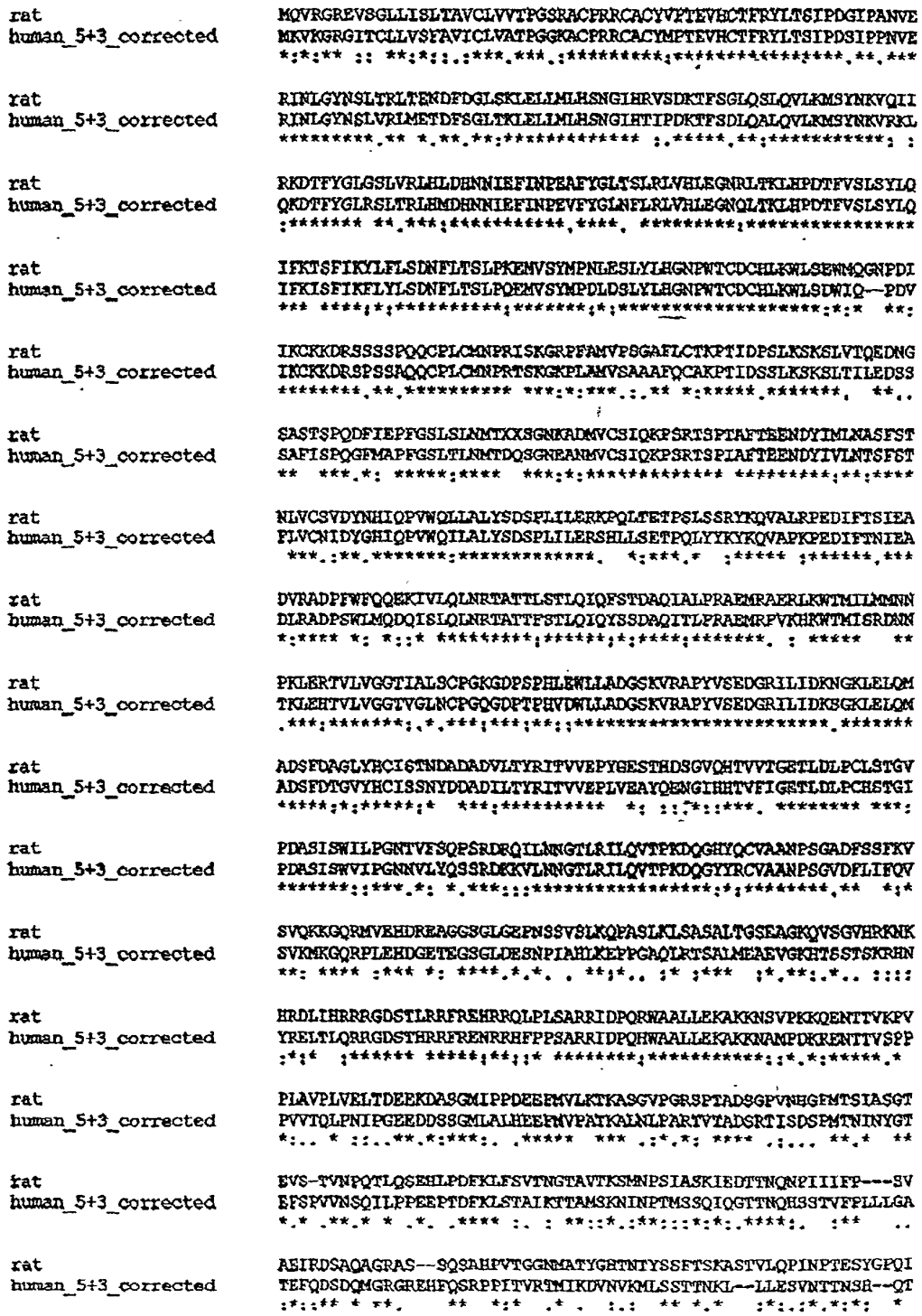
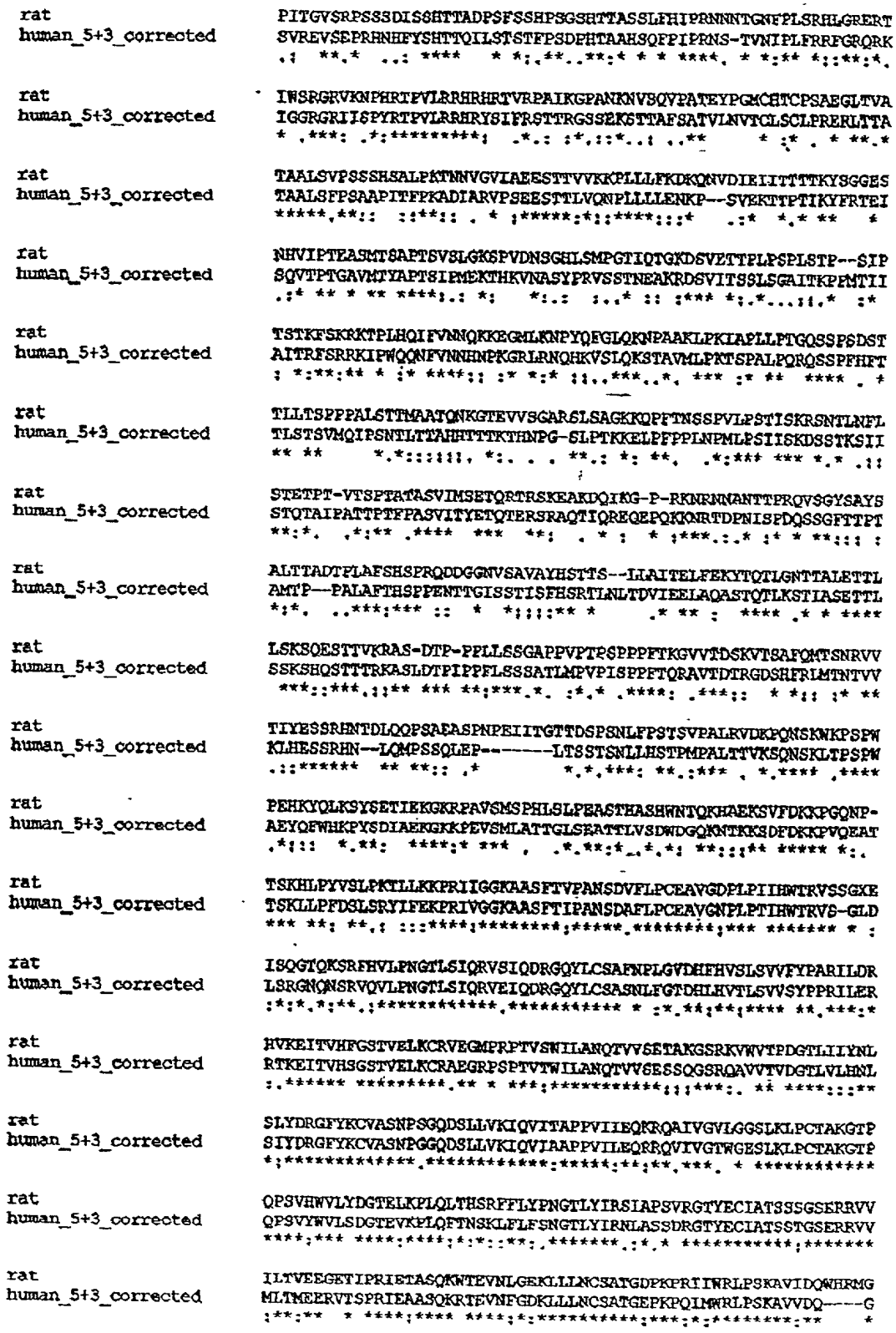


(rat: SEQ ID NO:10)
(human_5+3_corrected: SEQ ID NO:11)
(mouse_5_corrected: SEQ ID NO:12)

Figure 16




rat
human_5+3_corrected
rat
human_5+3_corrected
rat
human_5+3_corrected
rat
human_5+3_corrected
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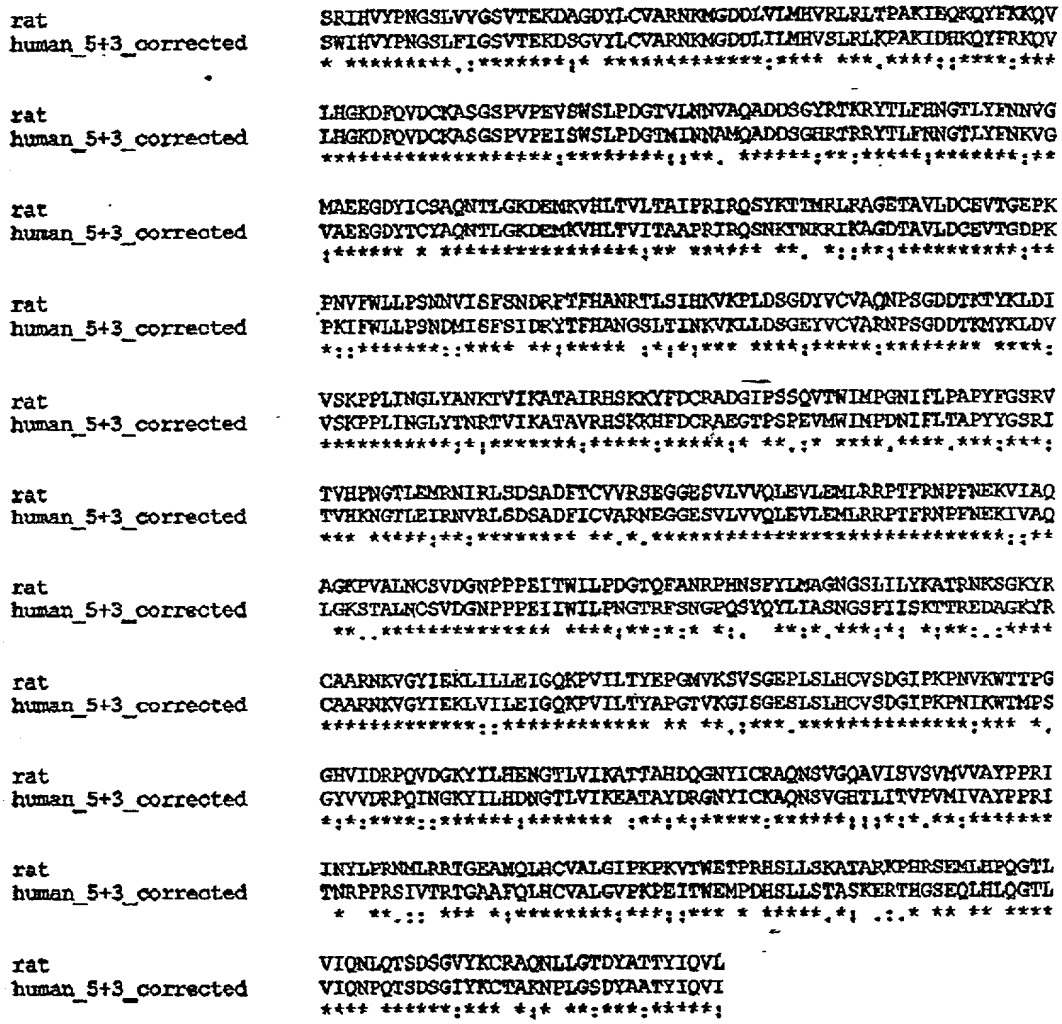
human_5+3_corrected



(rat: SEQ ID NO:13)
(human_5+3_corrected: SEQ ID NO:14)

Figure 17

MQKRGREVSCLLISLTAICLVVTPGSRVCPRRCACYVPTEVHCTFRDLTSIPDGPANVER
VNLGYNSLTRLTENDFSGLSRLELLMLHSNGIHRVSDKTFSGLQSLQVLKMSYNKVQIIE
KDTLYGLRSLTRLHLDHNNIEFINPEAFYGLTLLRLVHLEGNRLTKLHPDTFVSLSYLQIF
KTSFIKXLYLYDNFTSLPKEMVSSMPNLESLYLHGNPWTCDCHLKWLSEWMQGNP
(SEQ ID NO: 15)

Figure 18

MKVKGRGITCLLVSFAVICLVATPGGKACPRRCACYMPTEVHCTFRYLTSIPDSIPPNVE
RINLGYNSLVRLMETDFSGLTKLELLMLHSNGIHTIPDKTFSDLQALQVLKMSYNKVRK
LQKDTFYGLRSLTRLHMDHNNIEFINPEVFYGLNFLRLVHLEGNQLTKLHPDTFVSLSYL
QIFKISFIKFLYLSDNFLTSLPQEMSYMPDLDSLLYLHGNPWTCDCHLRWLSDWIQPDVI
KCKKDRSPSSAQQCPLCMNPRTSKGKPLAMVSAAAFQCAKPTIDSSLKSKSLTILEDSSS
AFISPQGFMAPFGSLTLNMTDQSGNEANMVCSIQKPSRTSPIAFTEENDYIVLNTSFSTFL
VCNIDYGHIQPVWQILALYSDSPLILERSHLLSETPQLYYKYKQVAPKPEDIFTNIEADLR
ADPSWLMQDQISLQLNRTATTFSTLQIQYSSDAQITLPRAEMRPVKHKWTMISRDNNTK
LEHTVLVGGTVGLNCPGQGDPTPHVDWLLADGSKVRAPYVSEDGRILIDKSGKLELQM
ADSFDTGVYHCISSNYDDADILTYRITVVEPLVEAYQENGIHHTVFIGETLDLPCHSTGIP
DASISWVIPGNNVLYQSSRDKKVLNNGTLRILQVTPKDQGYYRCVAANPSGVDFLIFQV
SVKMKGQRPLEHDGETEGSGLDESNPIAHLKEPPGAQLRTSALMEAEVGKHTSSTSKRH
NYRELTLQRRGDSTHRRFRENRRHFPPSARRIDPQHWAALLEKAKKNAMPDKRENTTV
SPPPVVTQLPNIPGEEDDSSGMLALHEEFMVPATKALNLPARTVTADSRTISDSPMTNIN
YGTEFSPVVNSQILPPEEPTDFKLSTAILTTAMSKNINPTMSSQIQGTTNQHSSTVFPLLLG
ATEFQDSDQMGRGREHFQSRPPITVRTMIKDVNVKMLSSTTNKLLLESVNSHQTSVREV
SEPRHNHFYSHTTQILSTSTFPSDPHTAAHSQFPIPRNSTVNIPLFRRFGRQRKIGGRGRIIS
PYRTPVLRRHRYSIFRSTTRGSSEKSTTAFSATVLNVTCLSCLPRELTTATAALSFPSAAPI
TFPKADIARVPSEESTTLVQNPLLLLENKPSVEKTTPTIKYFRTEISQVTPTGAVMTYAPT
SIPMEKTHKVNASYPRVSSTNEAKRDSVITSSLSGAITKPPMTIIAITRFSRRKIPWQQNFV
NNHNPKGRLRNQHKVSLQKSTAVMLPKTSPALPQRQSSPFHFRRLSTSVMQIPSNTLTT
AHHTTTKTHNPGSLPTKKELPFPPLNPMLPSIISKDSSTKSIISTQTAIPATTPTFPASVITYE
TQTERSRAQTIQREQEPQKKNRTDPNISPDQSSGFTTPTAMTPPALAFTHSPPENTTGISST
ISFHSRTLNLTDVIEELAQASTQTLKSTIASETTLSSKSHQSTTTRKASLDTPIPPFLSSSAT
LMPVPISPPFTQRAVTDTRGDSHFRLMTNTVVKLHESSRHNLQMPSSQLEPLTSSTSNLL
HSTPMPALTTVKSQNSKLTPSPWAEQFWHKPYSDIAEKGKKPEVSMLATTGLSEATTLV
SDWDGQKNTKKSDFDKKPVQEATTSKLLPFDSLSRYIFEKPRIVGGKAASFTIPANSDAF
LPCEAVGNPLPTIHWTRVSGLDLSRGNQNSRVQVLPNGTLSIQRVEIQDRFQYLCSASNL
FGTDHLHVTLSVVSYPPRILERRTKEITVHSGSTVELKCRAEGRPSPTVTWILANQTVVSE
SSQGSRQAVVTVDGTLVLHNLSIYDRGFYKCVASNPGGQDSLLVKIQVIAAPPVILEQRR
QVIVGTWGESLKLPCTAKGTPQPSVYWVLSDGTEVKPLQFTNSKLFLFSNGTLYIRNLAS

SDRFTYECIATSSTGSERRVVMLTMEERVTSPRIEAASQKRTEVNFGDKLLLNCSATGEP
KPQIMRLPSKAVVDQGSWIHYPNGSLFIGVTEKDSGVYLCVARNKMGDDLILMHVSLR
LKPAKIDHKQYFRKQVLHGKDFQVDCKASGSPVPEISWSLPDGTMINNAMQADDSGHR
TRRYRLFNNGTLYFNKVGVAEEGDYTCYAQNTLGKDEMKVHLTVITAAPRIRQSNKTN
KRIKAGDTAAVLDCEVTGDPKPKIFWLLPSNDMISFSIDRYTFHANGSLTINKVKLLDSG
EYVCVARNPSGDDTKMYKLDVVSKPPLINGLYTNRTVIKATAVRHSKKHFDCRAEGTP
SPEVMWIMPDNIFLTAPYYGSRITVHKNGTLEIRNVRLSADFICVARNEGGESVLVVQLE
VLEMLRRPTFRNPRNPFNEKIVAQLGKSTALNCVSVDGNPPPEIIWILPNGTRFSNGPQSY
QYLIASNGSFIISKTTREDAGKYRCAARNKVGYIEKLVILEIGQKPVILTYAPGTVKGISGE
SLSLHCVSDGIPKPNIKWTMPSGYVVDRPQINGKYILHDNGTLVIKEATAYDRGNYICKA
QNSVGHTLITVPVMIVAYPPRITNRPPRSIVTRTGAAFQLHCVALGVPKPEITWEMPDHS
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NO: 16)

Figure 19

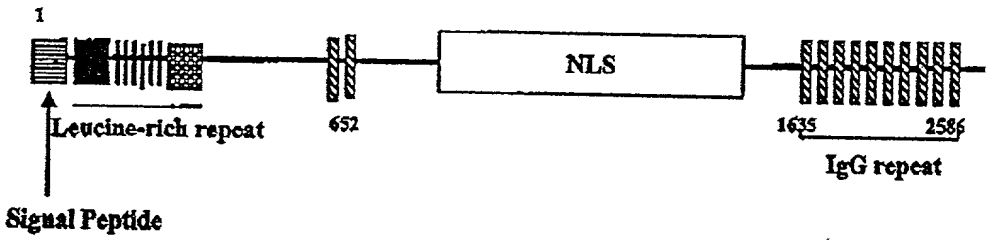
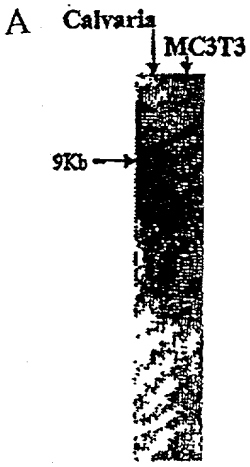


Figure 20

A



B

Cell lines & primary cells		
C6	Rat glioma	-
C2C12	Myoblasts	-
STO	Fibroblasts	-
Bone marrow	Stromal cells	- (+)
PC-3	prostatic carcinoma	-
SAOS-2	osteosarcoma	-
U2OS	osteosarcoma	+
Articular cartilage	chondrocytes	-
ROS	osteosarcoma	-
Calvaria	Osteoblasts	+
C3H10T1/2	mesenchyme	- (+)
MC3T3-E1	preosteoblastic	- (+)

Figure 21

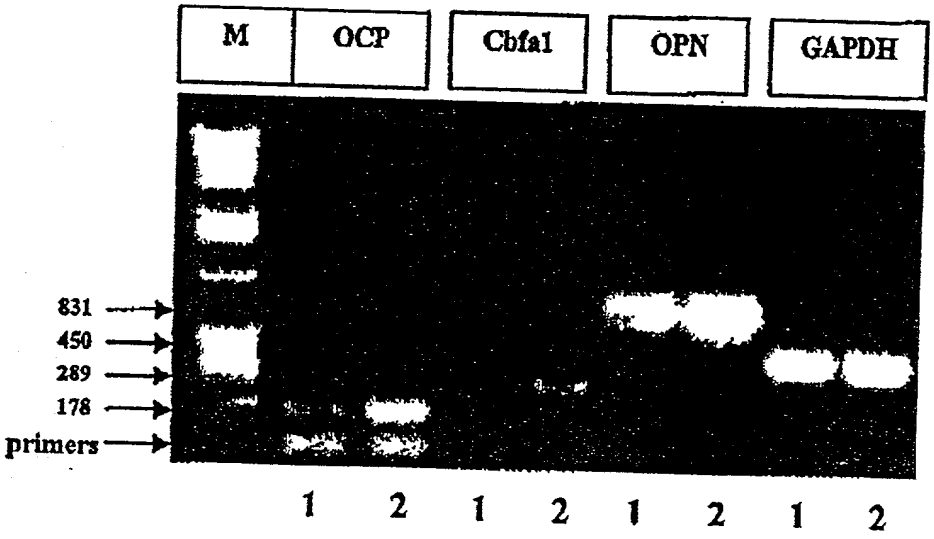


Figure 22

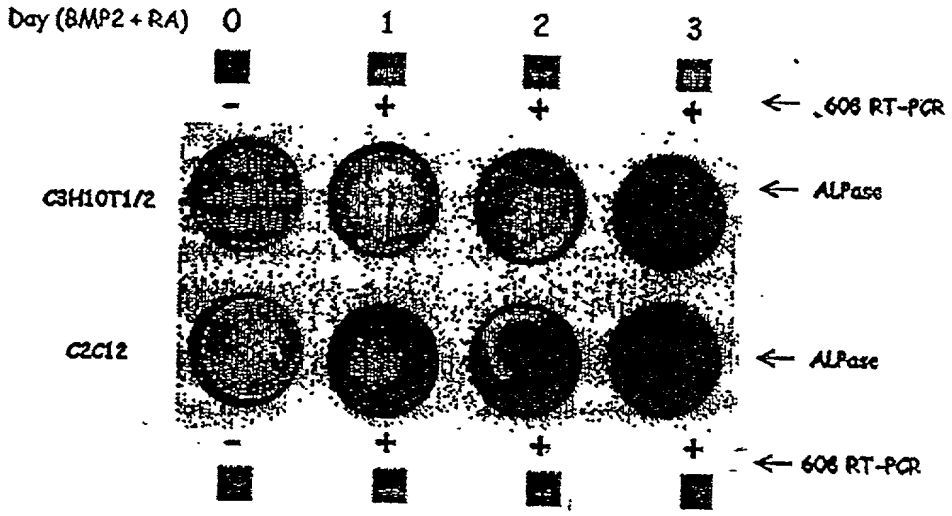


Figure 23

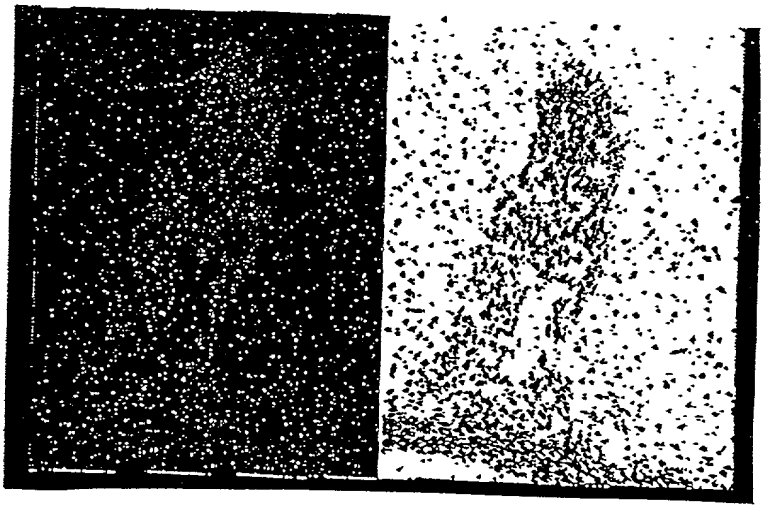


Figure 24

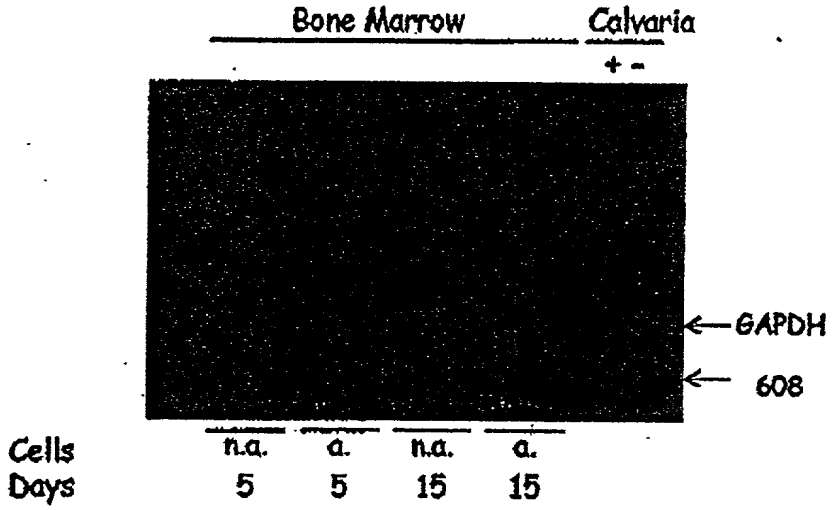


Figure 25

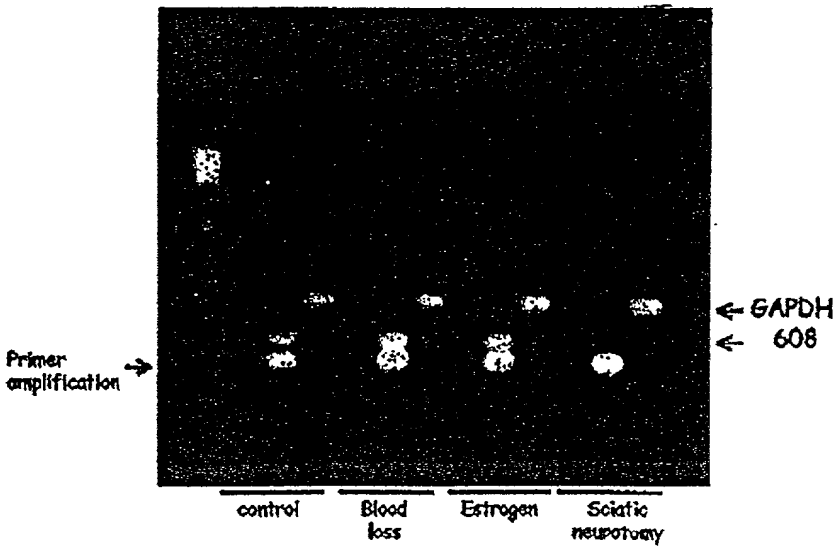


Figure 26

Figure 27

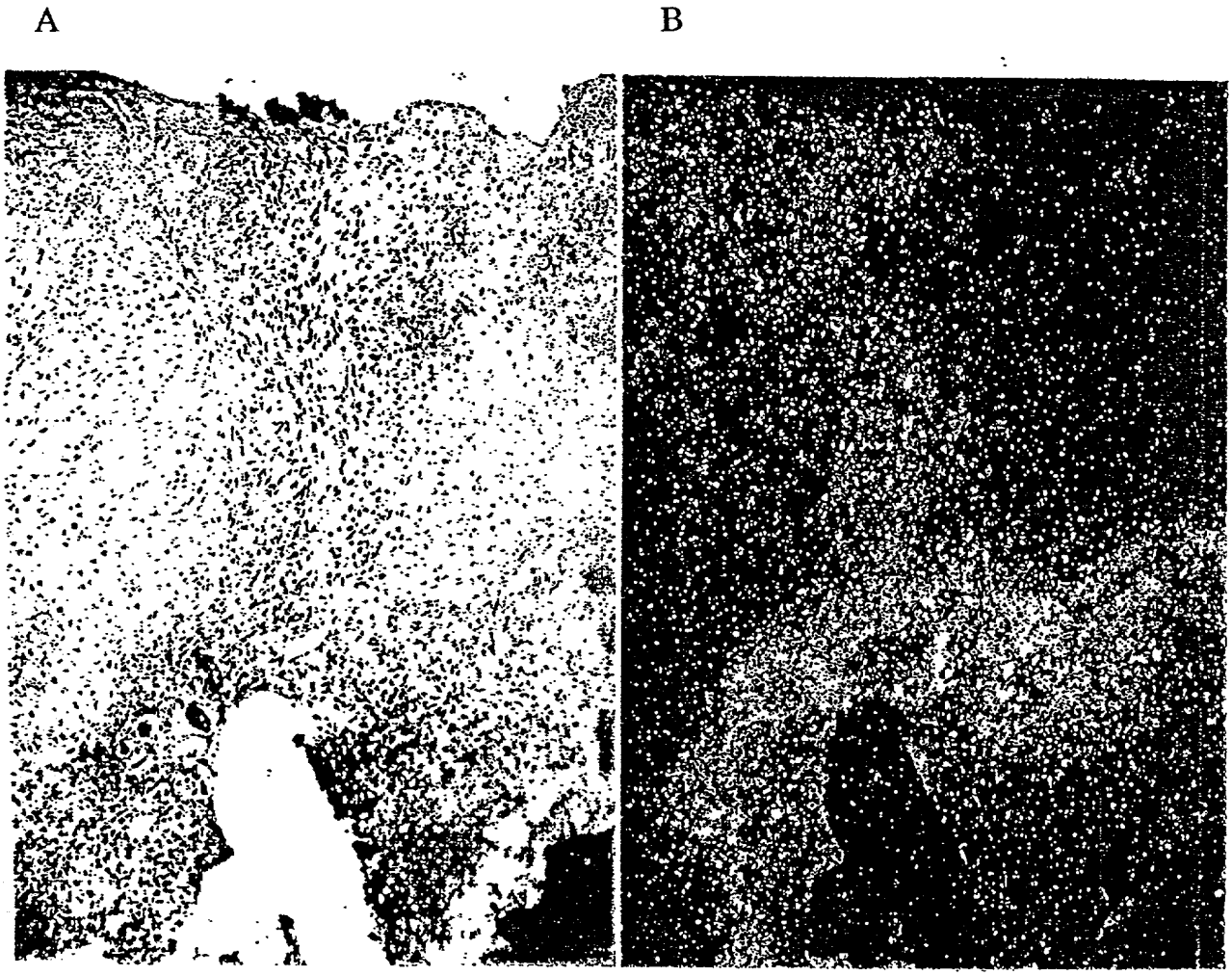
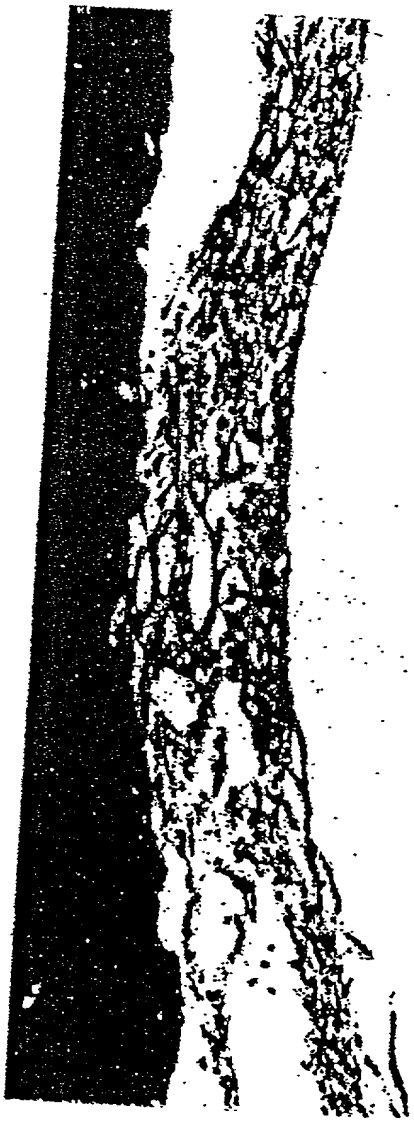


Figure 28

Figure 29

A



B

Figure 30

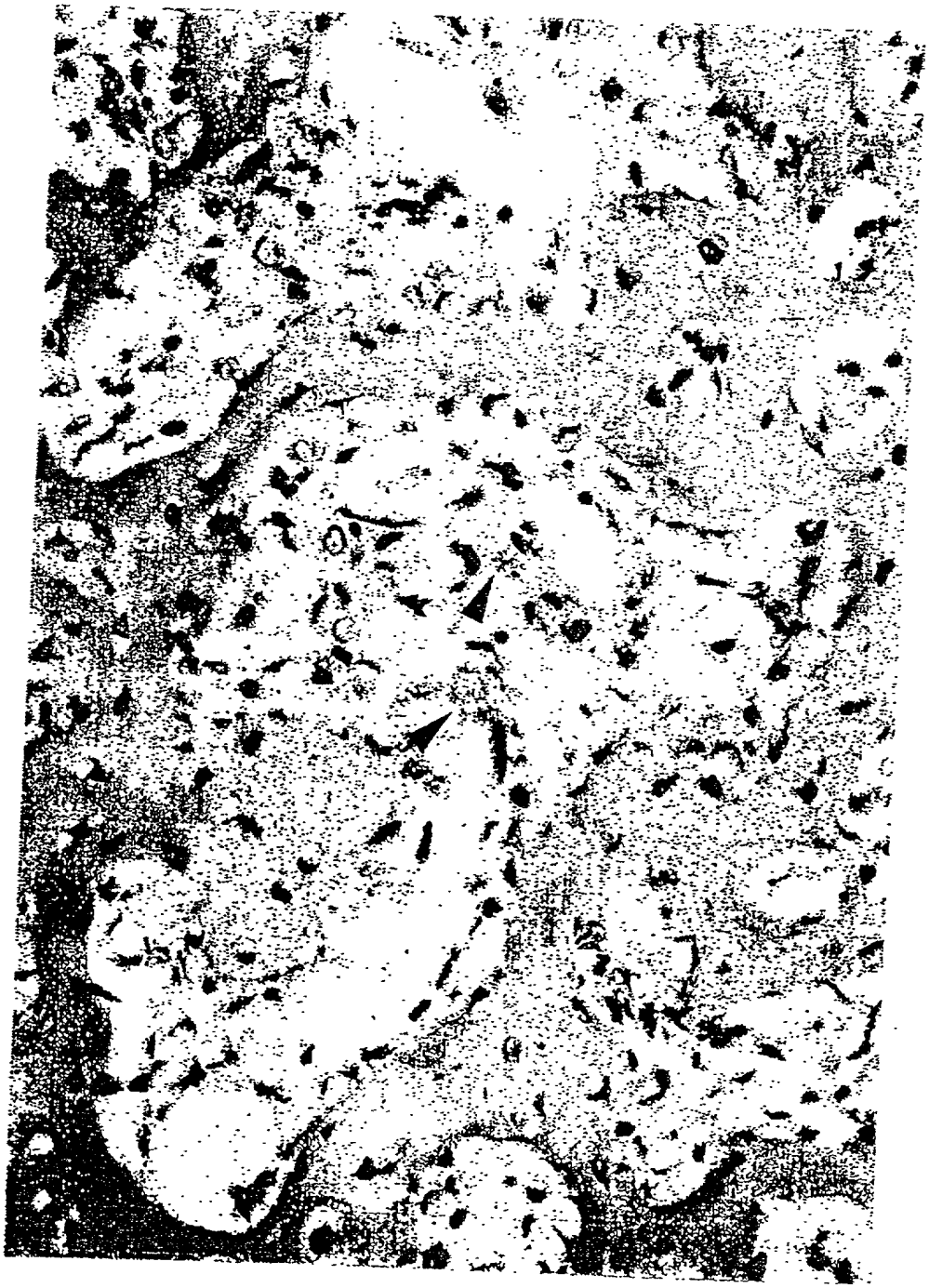
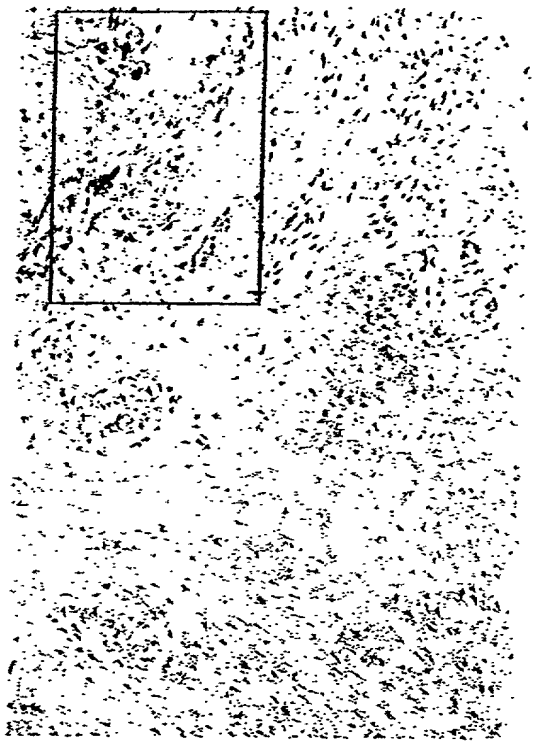


Figure 31

Figure 32

A



B

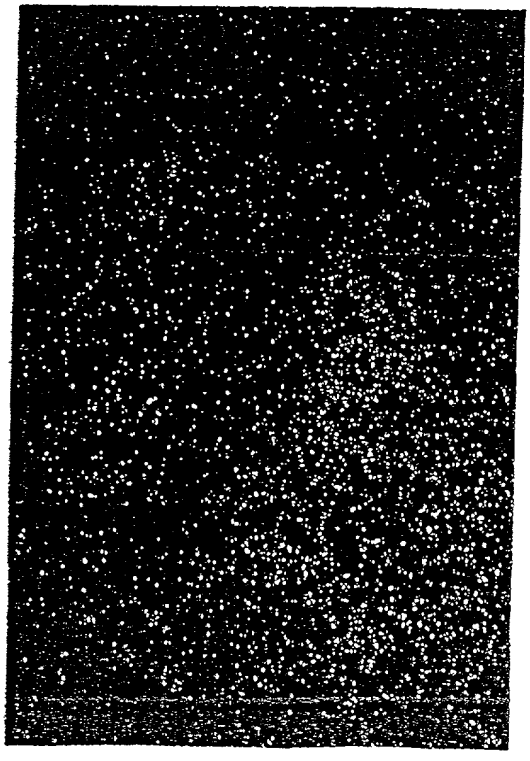


Figure 33

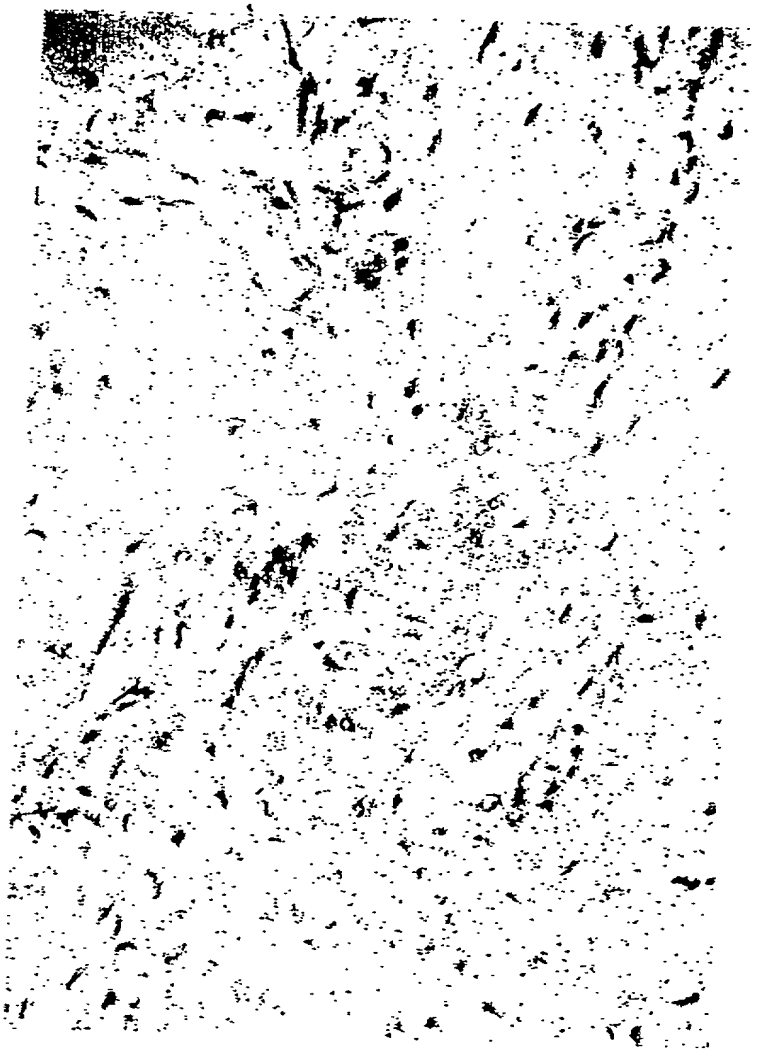


Figure 34

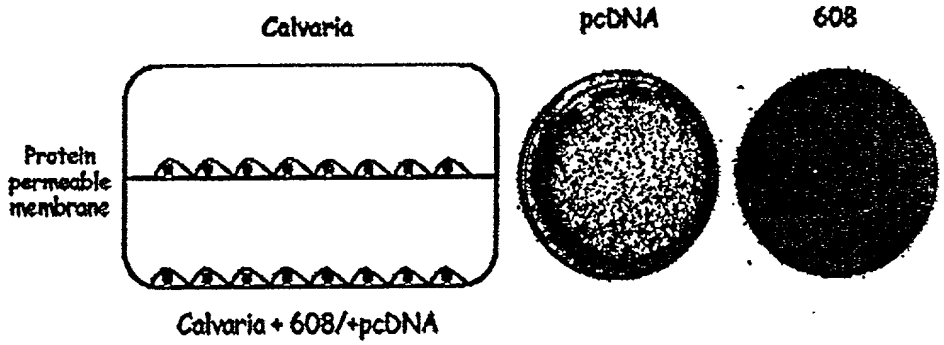


Figure 35

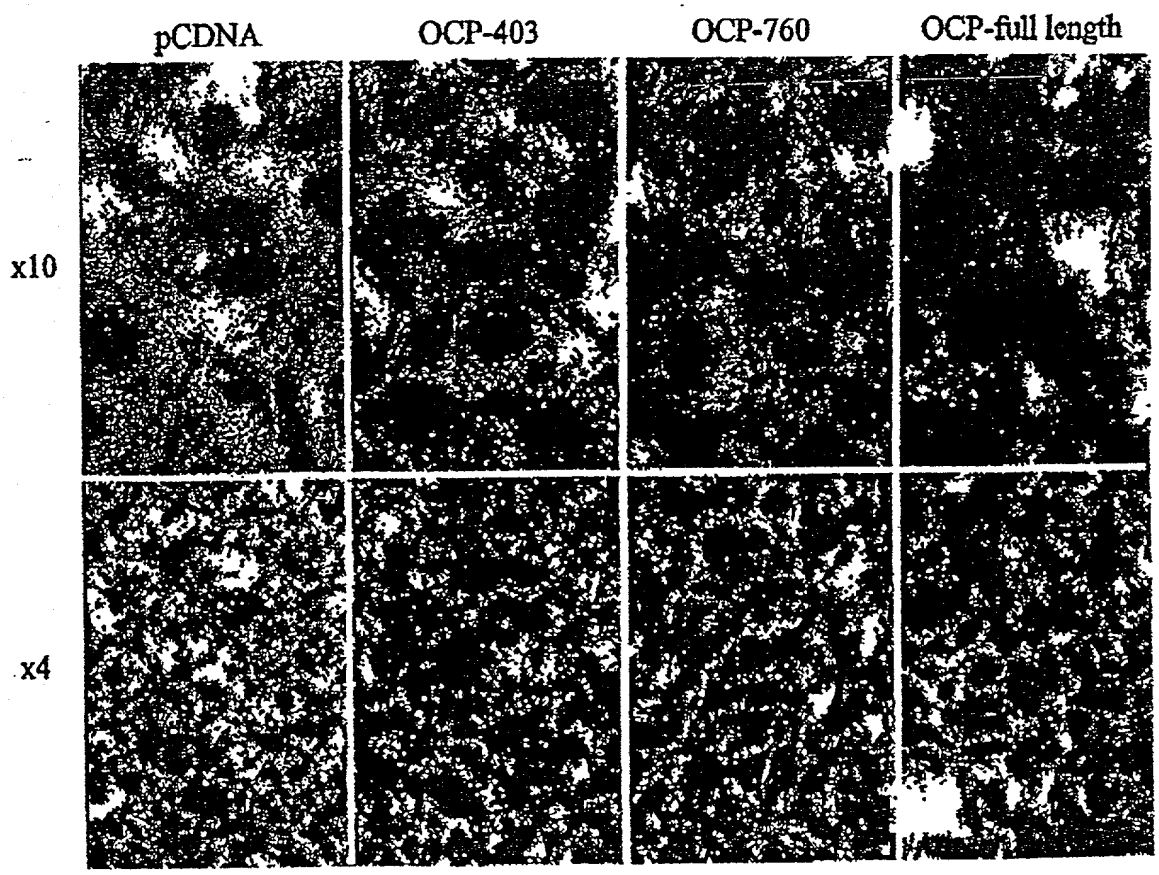


Figure 36

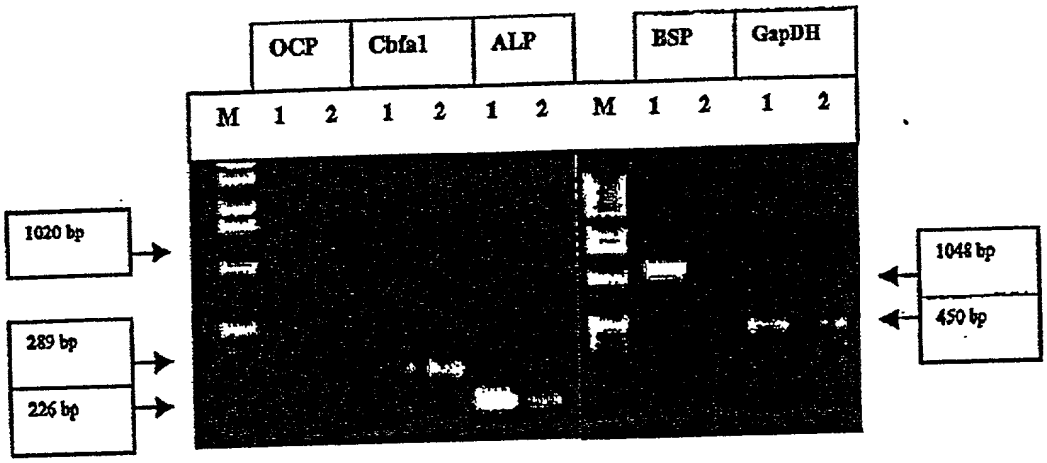


Figure 37

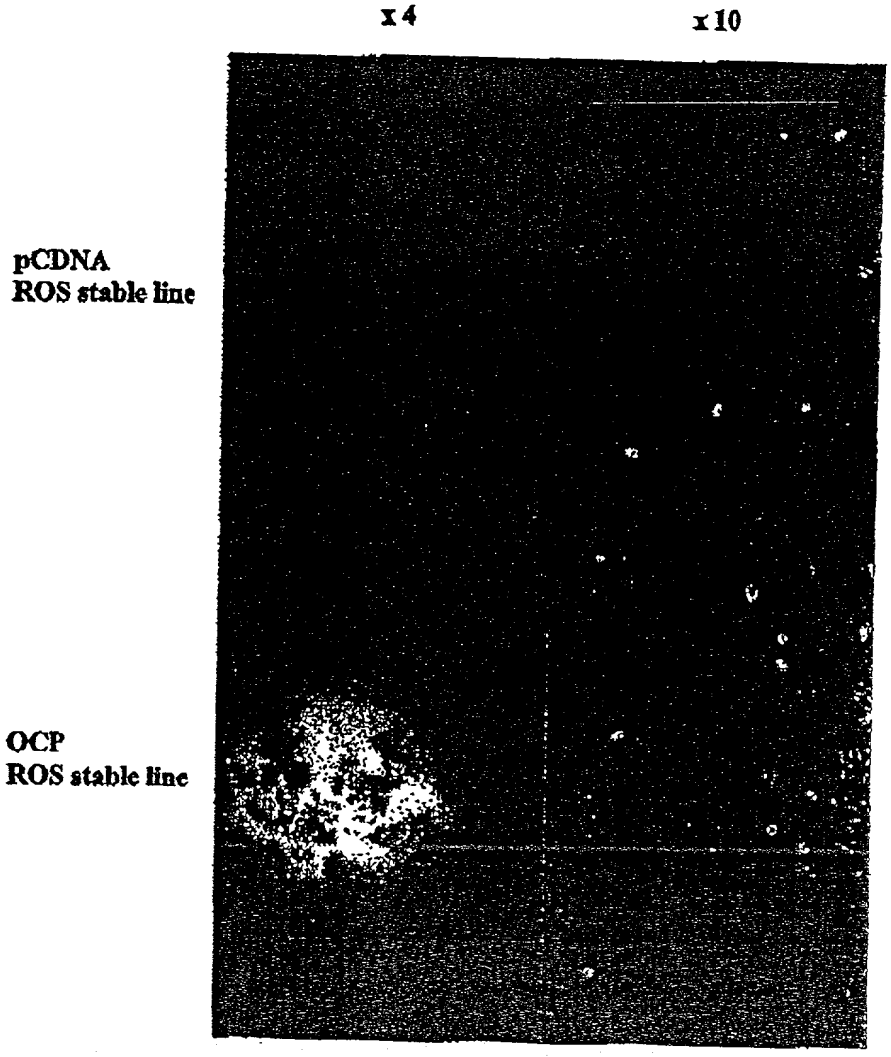


Figure 38

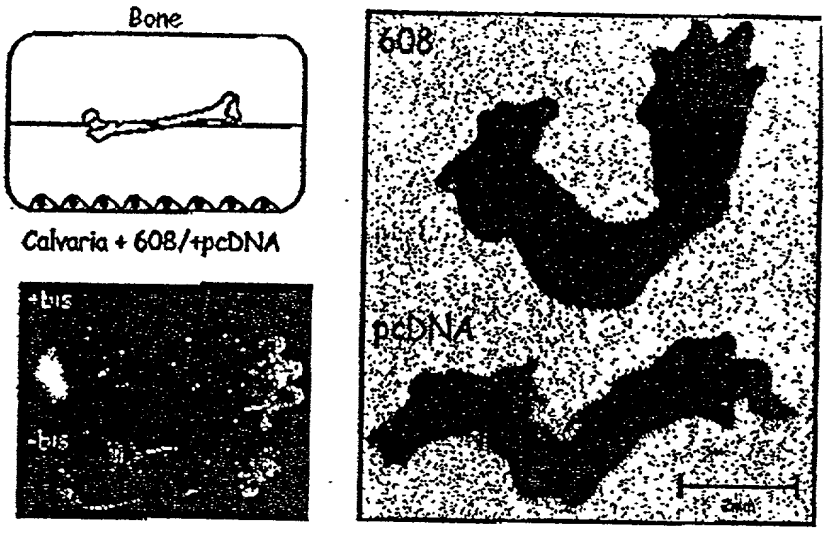


Figure 39

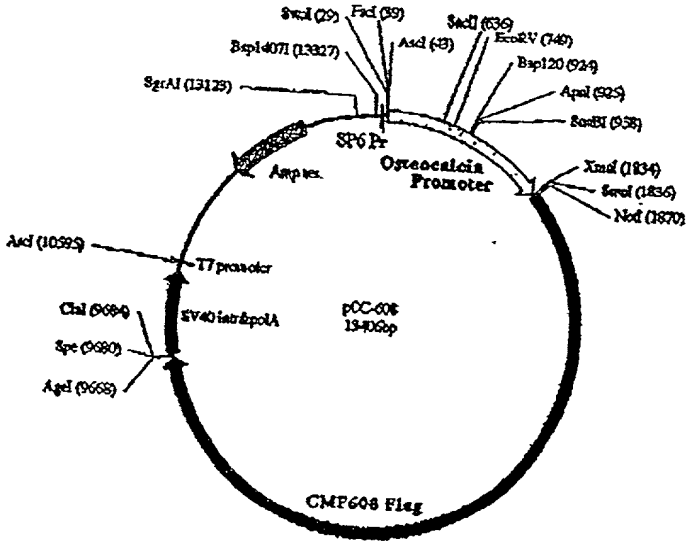


Figure 40

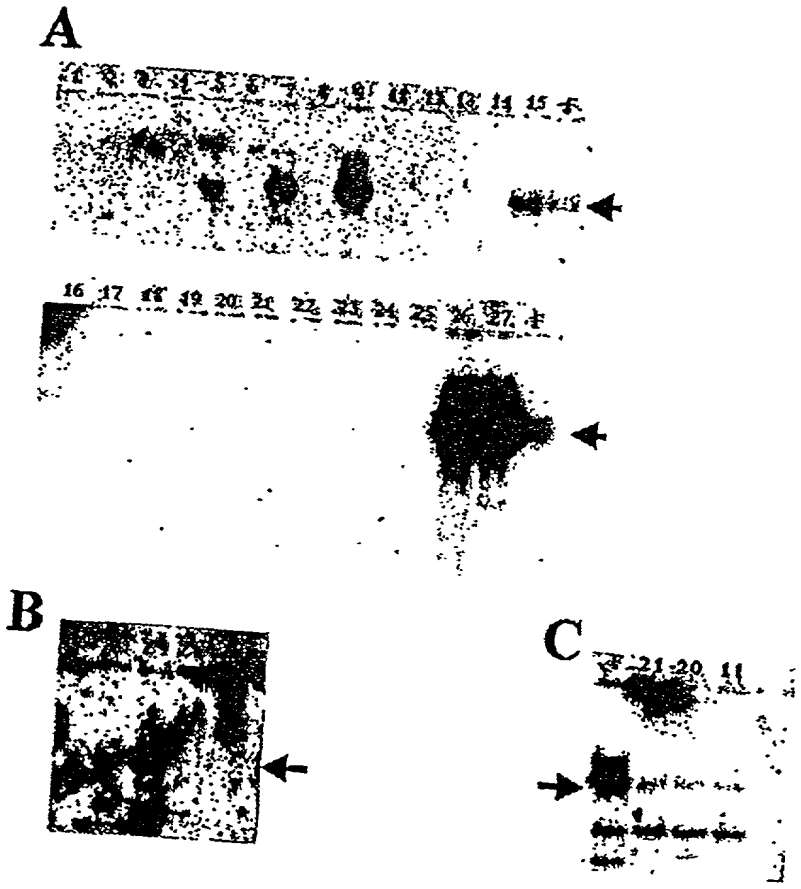
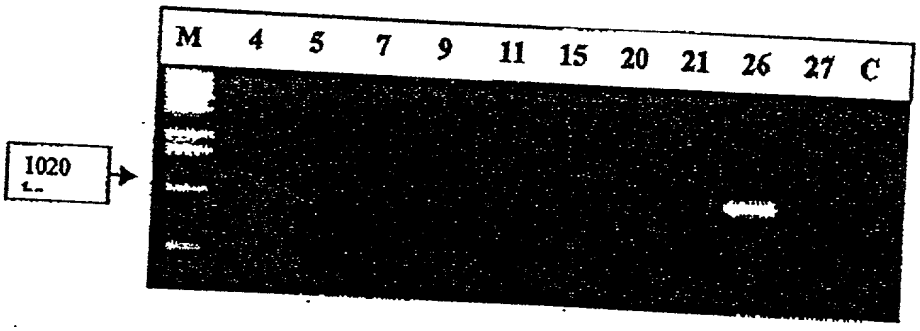


Figure 41

A



B

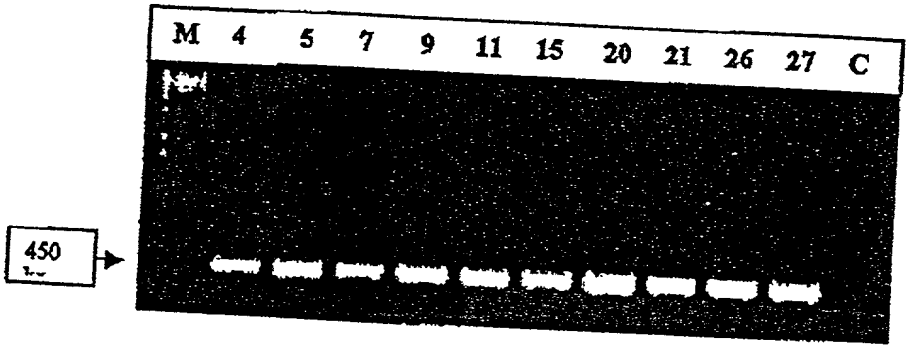
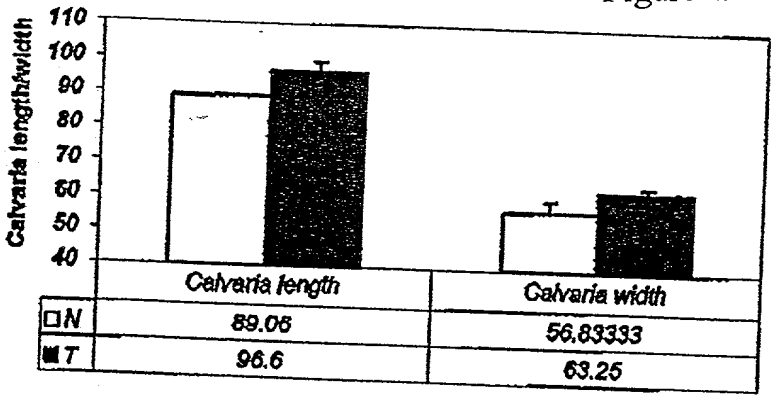


Figure 42

A



	Calvaria length	Calvaria width
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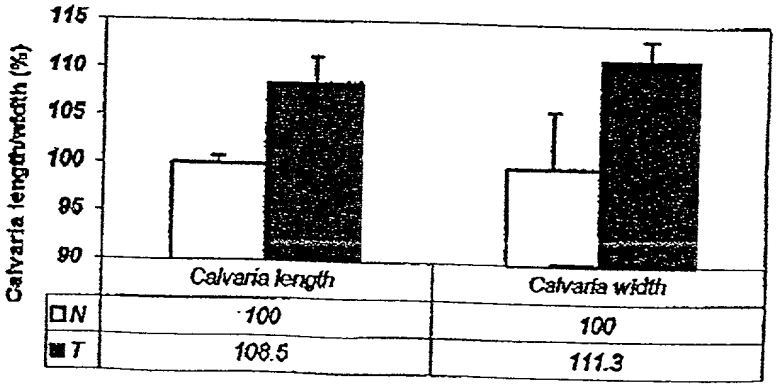
T	96.6	63.25

B



	Calvaria length	Calvaria width
N	100	100
T	108.5	111.3

Figure 43

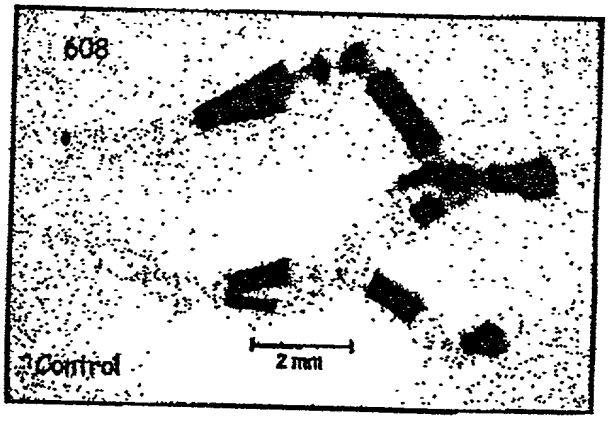


Figure 44

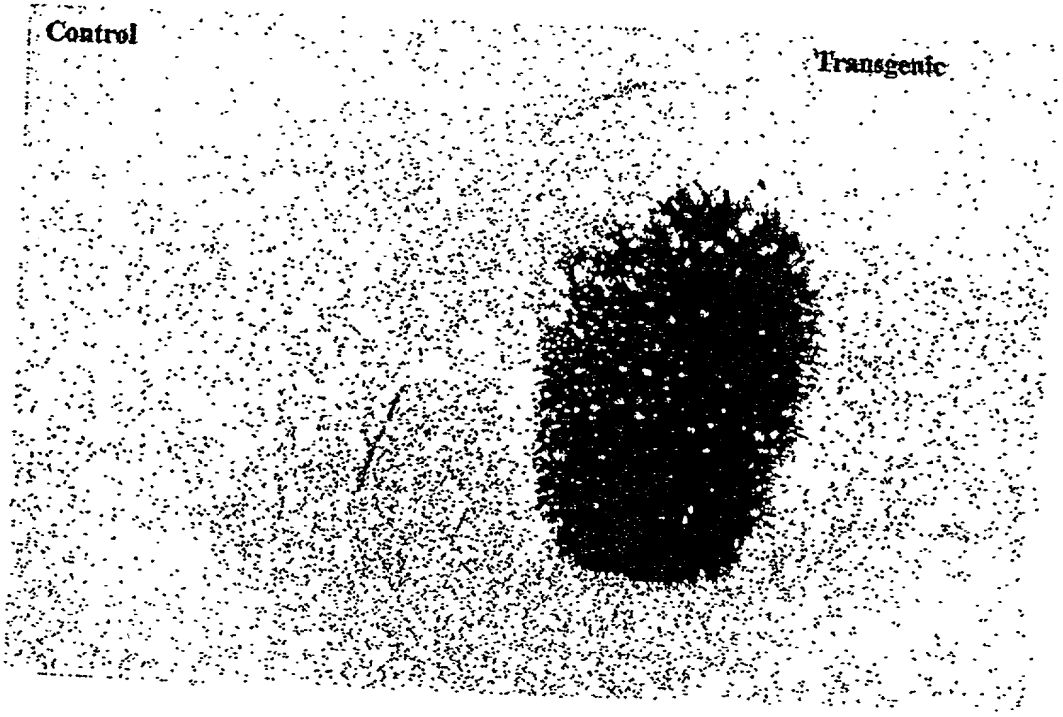
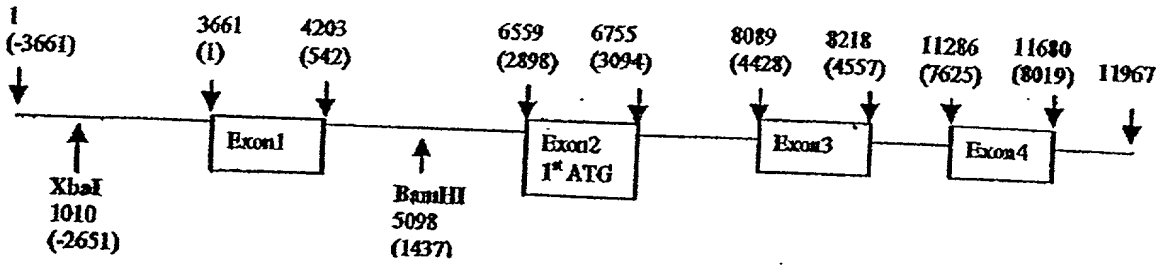


Figure 45



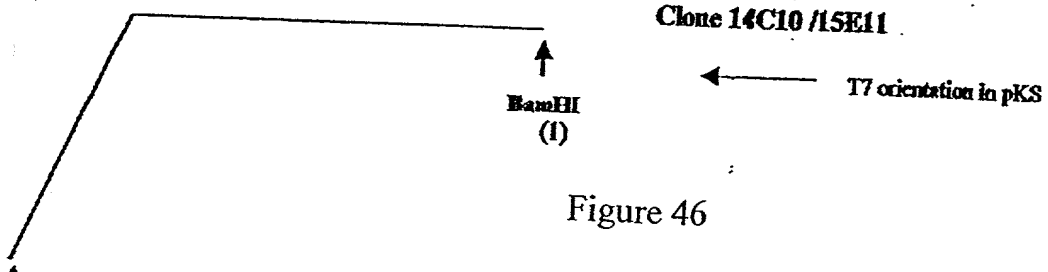


Figure 46

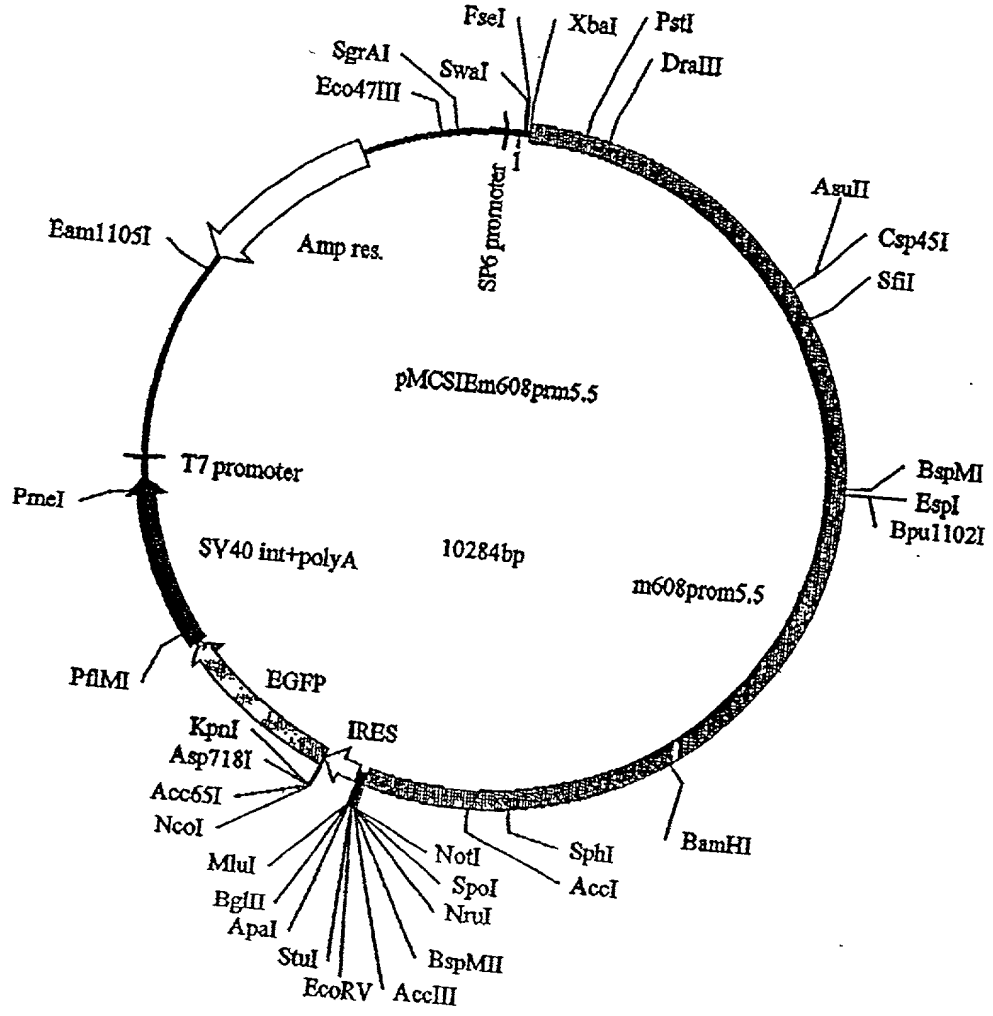
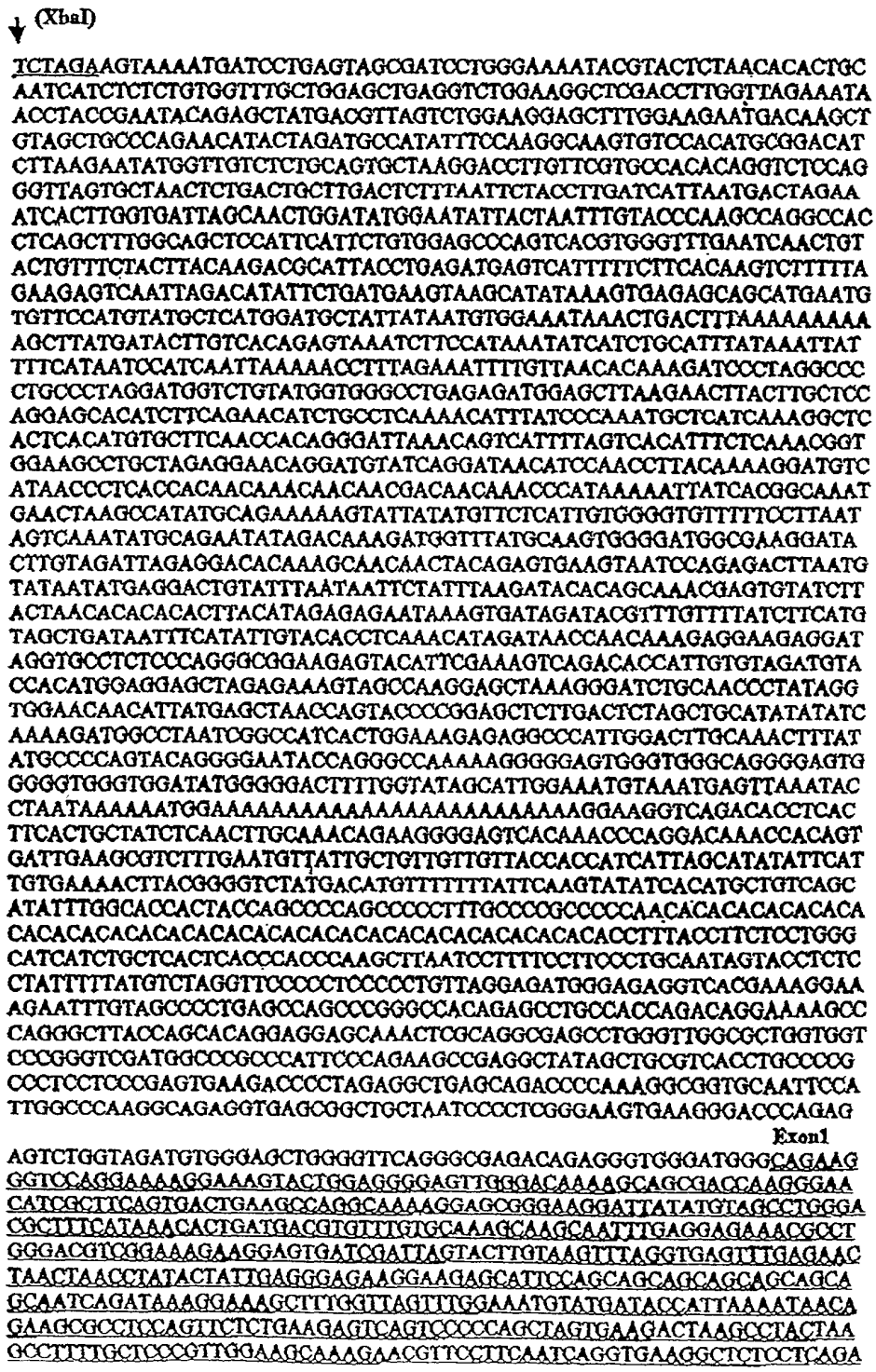


Figure 47



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NotI site

(SEQ ID NO:17)

Figure 48

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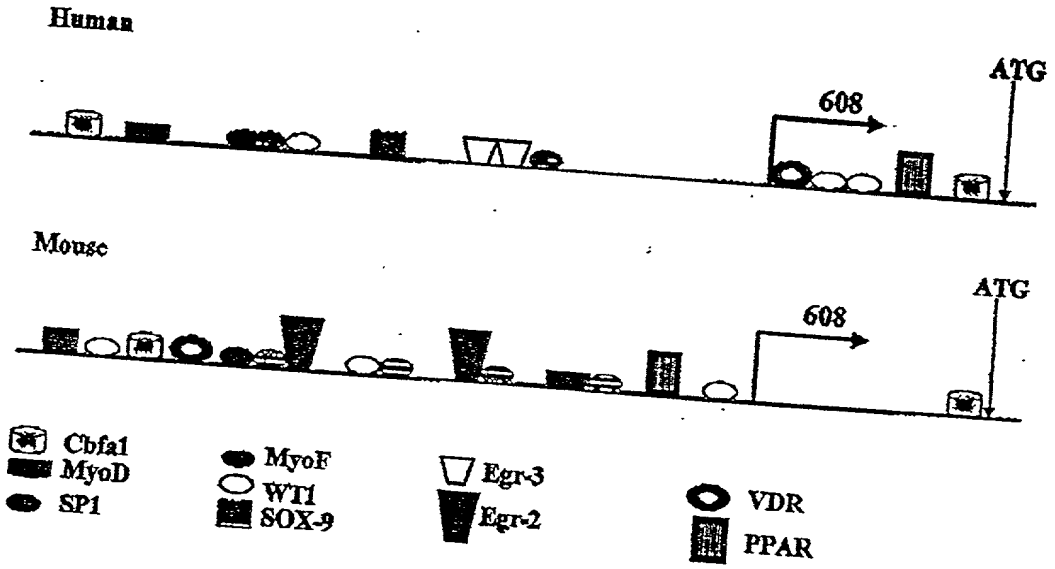
(SEQ ID NO:18)

Figure 49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ATG
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Cbfa1
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SP1
MyoF
WT1
SOX-9
Egr-3
Egr-2
VDR
PPAR

Figure 50

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GCAGAGGGGTGTTTCCAAGCAGAGAAAGAGCAGACAGTGTTATGCCTGCAAAGTCA
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CATTGGCCAAACACTCTATTCAATCAATGAAGTCCATATTCAGTGACAAAACTTGAC
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GCTCCGCTTGGTACATCTAGAAGGAAACCGGCTGACAAAGCTCCATCCAGACACAT
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TAGAAAGCCTTTACTTGCATGGAAACCCATGGACCTGTGACTGCCATTTAAAGTGGT
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TCCCCCCCCACTTCCCTACCTACCCATTCCCATTTTTTGGCCCTGGCATTCCCCTGTACT
GGGGCATATAAAGTTTGCGTGTCCAATGGACCTCTCTTTCCAGTGATGGCCAACTAG
GCCATCTTTTGATACATATGCAGCTAGAGTCAAGAGCTCTGGGGTACTGGTTAGTTC
ATAATGTTGTTGCACCTACAGGGTTGAA (SEQ ID NO:20)

Figure 51

MPKRAHWGALSVVLILLWGHPRVALACPHPCACYVPSEVHCTFRSLASVPAGIARHVE
RINLGFNSIQALSETSFAGLTKLELLMIHGNEIPSIPDGALRDLSSLQVFKFSYNKLRVITG
QTLQGLSNLMRLHIDHNKIEFIHPQAFNGLTSLRLLHLEGNLLHQLHPSTFSTFTFLDYFR
LSTIRHLYLAENMVRTLPASMLRNMPLLENLYLQGNPWTCDCEMRWFLEWDAKSRGIL
KCKKDKAYEGGQLCAMCFSPKKLYKHEIHKLKDMTCLKPSIESPLRQNRSRSIEEEQEQ
EEDGGSQLILEKFQLPQWSISLNMTDEHGNMVNLVCDIKKPMDVYKIHLNQTDPPDIDIN
ATVALDFECPMTRENYEKLWKLIAYYSEVPVKLHRELMLSKDPRVSYQYRQDADEEAL
YYTGVRAQILAEPEWVMQPSIDIQLNRRQSTAKKVLLSYYTQYSQTISTKDTRQARGRS
WVMIEPSGAVQRDQTVLEGGPCQLSCNVKASESPSIFWVLPDGSILKAPMDDPDSKFSIL
SSGWLRIKSMEPSDSGLYQCIAQVRDEMDRMVYRVLVQSPSTQPAEKDTVTIGKNPGES
VTLPCNALAIPEAHLSWILPNRRIINDLANTSHVYMLPNGTLSIPKVQVSDSGYYRCVAV
NQQGADHFTVGITVTKKGSGLPSKRGRRPGAKALSRVREDIVEDEGGSGMGDEENTSR
RLLHPKDQEVFLKTKDDAINGDKKAKKGRRKLKLWKHSEKEPETNVAEGRRVFESRRR
INMANKQINPERWADILAKVRGKNLPKGTEVPPLIKTTSPPSLSLEVTPPFPAVSPPSASP
VQTVTSAEESSADVPLLGEEEHVLGTISSASMGLEHNHNGVILVEPEVTSTPLEEVVDDL
SEKTEEITSTEGDLKGTAAPTLISEPYEPSPTLHTLDTVYEKPTHEETATEGWSAADVGSS
PEPTSSEYEPPLDAVSLAESEPMQYFDPDLETKSQPDEDKMKEDTFAHLTPTPTIWVNDS
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LEGDPTHSRSSESEGQESKSITLPDSTLGIMSSMSPVKKPAETTVGTLLDKDTTTVTTTPR
QKVAPSSTMSTHPSRRRPNGRRRLRPNKFRHRHKQTPPTTFAPSETFSTQPTQAPDIKISS
QVESSLVPTAWVDNTVNTPKQLEMEKNAEPTSKGTPRRKHGKRPNKHRYTPSTVSSRA
SGSKPSPSPENKHRNIVTPSSETILLPRTVSLKTEGPYDSLDYMTTTRKIYSSYPKVQETLP
VTYKPTSDGKEIKDDVATNVDKHKSDILVTGESITNAIPTSRSLVSTMGEFKEESSPVGFP
GTPTWNPSRTAQPGRLQTDIPVTTSGENLTDPPLLKELEDVDFTSEFLSSLTVSTPFHQEE
AGSSTTLSSIKVEVASSQAETTTLDQDHLETTVAILLSETRPQNHTPTAARMKEPASSSPS
TILMSLGQTTTTKPALPSPRISQASRDSKENVFLNYVGNPETEATPVNNEGTQHMSGPNE
LSTPSSDRDAFNLSTKLELEKQVFGSRSLPRGPDSQRQDGRVHASHQLTRVPAKPILPTA
TVRLPEMSTQSASRYFVTSQSPRHWTNKPEITTYPSGALPENKQFTTPRLSSTTIPLPLHM
SKPSIPSKFTDRRTDQFNGYSKVFGNNNIPEARNPVGKPPSPRIPHYSNGRLPFFTNKTLSF
PQLGVTRRPQIPTSPAPVMRERKVIPGSYNRIHSHSTFHLDFGPPAPPLLHTPQTTGSPSTN
LQNIPMVSSTQSSISFITSSVQSSGSFHQSSSKFFAGGPPASKFWSLGEKPQILTKSPQTVSV
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AALPPVIHQEKLENISLPPGLSIHIHCTAKAAPLPSVRWVLGDGTQIRPSQFLHGNLFVFP
NGTLYIRNLAPKDSGRYECVAANLVGSARRTVQLNVQRAAANARITGTSPRRTDVRYG
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DAGDYLCVARNKVGDDYVVLKVDVVMKPAKIEHKEENDHKVFYGGDLKVDCVATGL
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QVGKDEMRVRVKVVTAPATIRNKTYLAVQVPYGDVVTVACEAKGEPMPKVTWLSPTN
KVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGEDRKTVWIHVNVQPPKING
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RSLRKSDSVQLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGHTISLNCS
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GHTERLVSLKVGLKPEANKQYHNLVSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEG
PQTLGRVSLLDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPRITSEPTPVI
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QRDAGFYKCMAKNILGSDSKTTYIHVF (SEQ ID NO: 21)

Figure 52

ATGCCCAAGC GCGCGCACTG GGGGGCCCTC TCCGTGGTGC TGATCCTGCT
TTGGGGCCAT CCGCGAGTGG CGCTGGCCTG CCCGCATCCT TGTGCCTGCT
ACGTCCCCAG CGAGGTCCAC TGCACGTTCC GATCCCTGGC TTCCGTGCCC
GCTGGCATTG CTAGACACGT GGAAAGAATC AATTTGGGGT TTAATAGCAT
ACAGGCCCTG TCAGAAACCT CATTTGCAGG ACTGACCAAG TTGGAGCTAC
TTATGATTCA CGGCAATGAG ATCCCAAGCA TCCCCGATGG AGCTTTAAGA
GACCTCAGCT CTCTTCAGGT TTTCAAGTTC AGCTACAACA AGCTGAGAGT
GATCACAGGA CAGACCCTCC AGGGTCTCTC TAACTTAATG AGGCTGCACA
TTGACCACAA CAAGATCGAG TTTATCCACC CTCAAGCTTT CAACGGCTTA
ACGTCTCTGA GGCTACTCCA TTTGGAAGGA AATCTCCTCC ACCAGCTGCA
CCCCAGCACC TTCTCCACGT TCACATTTTT GGATTATTTC AGACTCTCCA
CCATAAGGCA CCTCTACTTA GCAGAGAACA TGGTTAGAAC TCTTCCTGCC
AGCATGCTTC GGAACATGCC GCTTCTGGAG AATCTTTACT TGCAGGGAAA
TCCGTGGACC TGCGATTGTG AGATGAGATG GTTTTTGGAA TGGGATGCAA
AATCCAGAGG AATTCTGAAG TGTAAAAAGG ACAAAGCTTA TGAAGGCGGT
CAGTTGTGTG CAATGTGCTT CAGTCCAAAG AAGTTGTACA AACATGAGAT
ACACAAGCTG AAGGACATGA CTTGTCTGAA GCCTTCAATA GAGTCCCCTC
TGAGACAGAA CAGGAGCAGG AGTATTGAGG AGGAGCAAGA ACAGGAAGAG
GATGGTGGCA GCCAGCTCAT CCTGGAGAAA TTCCAACTGC CCCAGTGGAG
CATCTCTTTG AATATGACCG ACGAGCACGG GAACATGGTG AACTTGGTCT
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GATCCTCCAG ATATTGACAT AAATGCAACA GTTGCCTTGG ACTTTGAGTG
TCCAATGACC CGAGAAAACT ATGAAAAGCT ATGGAAATTG ATAGCATACT
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AGCCATCCAT AGATATCCAG CTGAACCGAC GTCAGAGTAC GGCCAAGAAG
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CTGTGCAAAG AGATCAGACT GTCCTGGAAG GGGGTCCATG CCAGTTGAGC
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TGGCTCCATC CTGAAAGCGC CCATGGATGA CCCAGACAGC AAGTTCTCCA
TTCTCAGCAG TGGCTGGCTG AGGATCAAGT CCATGGAGCC ATCTGACTCA
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GATAATTAAT GATTTGGCTA ACACATCACA TGTATACATG TTGCCAAATG
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ACACCAAGGC AAAAAGTTGC TCCGTCATCC ACCATGAGCA CTCACCCTTC
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CGGAGAAAAC ACGGGAAGAG GCCAAACAAA CATCGATATA CCCCTTCTAC
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AACATAGAAA CATTGTTACT CCCAGTTCAG AAACTATACT TTTGCCTAGA
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CAGTCACATA

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TGGGGAATCC AGAAACAGAA GCAACCCCAG TCAACAATGA AGGAACACAG
CATATGTCAG GGCCAAATGA ATTATCAACA CCCTCTTCCG ACCGGGATGC
ATTTAACTTG TCTACAAAGC TGGAATTGGA AAAGCAAGTA TTTGGTAGTA
GGAGTCTACC ACGTGGCCCA GATAGCCAAC GCCAGGATGG AAGAGTTCAT
GCTTCTCATC AACTAACCAG AGTCCCTGCC AAACCCATCC TACCAACAGC
AACAGTGAGG CTACCTGAAA TGTCCACACA AAGCGCTTCC AGATACTTTG
TAACTTCCCA GTCACCTCGT CACTGGACCA ACAAACCGGA AATAACTACA
TATCCTTCTG GGGCTTTGCC AGAGAACAAA CAGTTTACAA CTCCAAGATT
ATCAAGTACA ACAATTCCTC TCCCATTGCA CATGTCCAAA CCCAGCATTC
CTAGTAAGTT TACTGACCGA AGAACTGACC AATTCAATGG TTACTCCAAA
GTGTTTGGAA ATAACAACAT CCCTGAGGCA AGAAACCCAG TTGGAAAGCC
TCCCAGTCCA AGAATTCCTC ATTATTCCAA TGGAAGACTC CCTTTCTTTA
CCAACAAGAC TCTTTCTTTT CCACAGTTGG GAGTCACCCG GAGACCCCAG
ATACCCACTT CTCCTGCCCC AGTAATGAGA GAGAGAAAAG TTATTCCAGG
TTCCTACAAC AGGATACATT CCCATAGCAC CTTCCATCTG GACTTTGGCC
CTCCGGCACC TCCGTTGTTG CACACTCCGC AGACCACGGG ATCACCCTCA
ACTAACTTAC AGAATATCCC TATGGTCTCT TCCACCCAGA GTTCTATCTC
CTTTATAACA TCTTCTGTCC AGTCCTCAGG AAGCTTCCAC CAGAGCAGCT
CAAAGTTCTT TGCAGGAGGA CCTCCTGCAT CCAAATTCTG GTCTCTTGGG
GAAAAGCCCC AAATCCTCAC CAAGTCCCCA CAGACTGTGT CCGTCACCGC
TGAGACAGAC ACTGTGTTCC CCTGTGAGGC AACAGGAAAA CCAAAGCCTT
TCGTTACTTG GACAAAGGTT TCCACAGGAG CTCTTATGAC TCCGAATACC
AGGATACAAC GGTTTGAGGT TCTCAAGAAC GGTACCTTAG TGATACGGAA
GGTTCAAGTA CAAGATCGAG GCCAGTATAT GTGCACCGCC AGCAACCTGC
ACGGCCTGGA CAGGATGGTG GTCTTGCTTT CGGTCACCGT GCAGCAACCT
CAAATCCTAG CCTCCCACTA CCAGGACGTC ACTGTCTACC TGGGAGACAC
CATTGCAATG GAGTGTCTGG CCAAAGGGAC CCCAGCCCCC CAAATTTCCT
GGATCTTCCC TGACAGGAGG GTGTGGCAAA CTGTGTCCCC

CGTGGAGAGC CGCATCACCC TGCACGAAAA CCGGACCCTT TCCATCAAGG
AGGCGTCCTT CTCAGACAGA GGCGTCTATA AGTGCGTGGC CAGCAATGCA
GCCGGGGCGG ACAGCCTGGC CATCCGCCTG CACGTGGCGG CACTGCCCCC
CGTTATCCAC CAGGAGAAGC TGGAGAACAT CTCGCTGCCC CCGGGGCTCA
GCATTCACAT TCACTGCACT GCCAAGGCTG CGCCCCTGCC CAGCGTGCGC
TGGGTGCTCG GGGACGGTAC CCAGATCCGC CCCTCGCAGT TCCTCCACGG
GAACTTGTTT GTTTTCCCCA ACGGGACGCT CTACATCCGC AACCTCGCGC
CCAAGGACAG CGGGCGCTAT GAGTGCGTGG CCGCCAACCT GGTAGGCTCC
GCGCGCAGGA CGGTGCAGCT GAACGTGCAG CGTGCAGCAG CCAACGCGCG
CATCACGGGC ACCTCCCCGC GGAGGACGGA CGTCAGGTAC GGAGGAACCC
TCAAGCTGGA CTGCAGCGCC TCGGGGGACC CCTGGCCGCG CATCCTCTGG
AGGCTGCCGT CCAAGAGGAT GATCGACGCG CTCTTCAGTT TTGATAGCAG
AATCAAGGTG TTTGCCAATG GGACCCTGGT GGTGAAATCA GTGACGGACA
AAGATGCCGG AGATTACCTG TGCGTAGCTC GAAATAAGGT TGGTGATGAC
TACGTGGTGC TCAAAGTGGA TGTGGTGATG AAACCGGCCA AGATTGAACA
CAAGGAGGAG AACGACCACA AAGTCTTCTA CGGGGGTGAC CTGAAAGTGG
ACTGTGTGGC CACCGGGCTT CCCAATCCCG AGATCTCCTG GAGCCTCCCA
GACGGGAGTC TGGTGAACTC CTTCATGCAG TCGGATGACA GCGGTGGACG
CACCAAGCGC TATGTCGTCT TCAACAATGG GACACTCTAC TTTAACGAAG
TGGGGATGAG GGAGGAAGGA GACTACACCT GCTTTGCTGA AAATCAGGTC
GGGAAGGACG AGATGAGAGT CAGAGTCAAG GTGGTGACAG CGCCCGCCAC
CATCCGGAAC AAGACTTACT TGGCGGTTCA GGTGCCCTAT GGAGACGTGG
TCACTGTAGC CTGTGAGGCC AAAGGAGAAC CCATGCCCAA GGTGACTTGG
TTGTCCCCAA CCAACAAGGT GATCCCCACC TCCTCTGAGA AGTATCAGAT
ATACCAAGAT GGCACTCTCC TTATTCAGAA AGCCCAGCGT TCTGACAGCG
GCAACTACAC CTGCCTGGTC AGGAACAGCG CGGGAGAGGA TAGGAAGACG
GTGTGGATTC ACGTCAACGT CCAGCCACCC AAGATCAACG GTAACCCCAA
CCCCATCACC ACCGTGCGGG AGATAGCAGC CGGGGGCAGT CGGAAACTGA
TTGACTGCAA AGCTGAAGGC ATCCCCACCC CGAGGGTGTT ATGGGCTTTT
CCCGAGGGTG TGGTTCTGCC AGCTCCATAC TATGGAAACC GGATCACTGT
CCATGGCAAC GGTTCCCTGG ACATCAGGAG TTTGAGGAAG AGCGACTCCG
TCCAGCTGGT ATGCATGGCA CGCAACGAGG GAGGGGAGGC GAGGTTGATC
GTGCAGCTCA CTGTCCTGGA GCCCATGGAG AAACCCATCT TCCACGACCC
GATCAGCGAG AAGATCACGG CCATGGCGGG CCACACCATC AGCCTCAACT
GCTCTGCCGC GGGGACCCCG ACACCCAGCC TGGTGTGGGT CCTTCCCAAT
GGCACCGATC TGCAGAGTGG ACAGCAGCTG CAGCGCTTCT ACCACAAGGC
TGACGGCATG CTACACATTA GCGGTCTCTC CTCGGTGGAC GCTGGGGCCT
ACCGCTGCGT GGCCCGCAAT GCCGCTGGCC ACACGGAGAG GCTGGTCTCC
CTGAAGGTGG GACTGAAGCC AGAAGCAAAC AAGCAGTATC ATAACCTGGT
CAGCATCATC AATGGTGAGA CCCTGAAGCT CCCCTGCACC CCTCCCGGGG
CTGGGCAGGG ACGTTTCTCC TGGACGCTCC CCAATGGCAT GCATCTGGAG

GGCCCCCAAA CCCTGGGACG CGTTTCTCTT CTGGACAATG GCACCCTCAC
GGTTCGTGAG GCCTCGGTGT TTGACAGGGG TACCTATGTA TGCAGGATGG
AGACGGAGTA CGGCCCTTCG GTCACCAGCA TCCCCGTGAT TGTGATCGCC
TATCCTCCCC GGATCACCAG CGAGCCCACC CCGGTCATCT ACACCCGGCC
CGGGAACACC GTGAAACTGA ACTGCATGGC TATGGGGATT CCCAAAGCTG
ACATCACGTG GGAGTTACCG GATAAGTCGC ATCTGAAGGC AGGGGTTCAG
GCTCGTCTGT ATGGAAACAG ATTTCTTCAC CCCCAGGGAT CACTGACCAT
CCAGCATGCC ACACAGAGAG ATGCCGGCTT CTACAAGTGC ATGGCAAAAA
ACATTCTCGG CAGTGACTCC AAAACAACTT ACATCCACGT CTTCTGAAAT
GTGGATTCCA GAATGATTGC TTAGGAACTG ACAACAAAGC GGGGTTTGTA
AGGGAAGCCA GGTTGGGGAA TAGGAGCTCT TAAATAATGT GTCACAGTGC
ATGGTGGCCT CTGGTGGGTT TCAAGTTGAG GTTGATCTTG ATCTACAATT
GTTGGGAAAA GGAAGCAATG CAGACACGAG AAGGAGGGCT CAGCCTTGCT
GAGACACTTT CTTTTGTGTT TACATCATGC CAGGGGCTTC ATTCAGGGTG
TCTGTGCTCT GACTGCAATT TTTCTTCTTT TGCAAATGCC ACTCGACTGC
CTTCATAAGC GTCCATAGGA TATCTGAGGA ACATTCATCA AAAATAAGCC
ATAGACATGA ACAACACCTC ACTACCCCAT TGAAGACGCA TCACCTAGTT
AACCTGCTGC AGTTTTTACA TGATAGACTT TGTTCCAGAT TGACAAGTCA
TCTTTCAGTT ATTTCCTCTG TCACTTCAAA ACTCCAGCTT GCCCAATAAG
GATTTAGAAC CAGAGTGACT GATATATATA TATATATTTT AATTCAGAGT
TACATACATA CAGCTACCAT TTTATATGAA AAAAGAAAAA CATTTCTTCC
TGGAACTCAC TTTTTATATA ATGTTTTATA TATATATTTT TTCCTTTCAA
ATCAGACGAT GAGACTAGAA GGAGAAATAC TTTCTGTCTT ATTAAAATTA
ATAAATTATT GGTCTTTACA AGACTTGGAT ACATTACAGC AGACATGGAA
ATATAATTTT AAAAAATTTC TCTCCAACCT CCTTCAAATT CAGTCACCAC
TGTTATATTA CCTTCTCCAG GAACCCTCCA GTGGGGAAGG CTGCGATATT
AGATTTCCTT GTATGCAAAG TTTTTGTTGA AAGCTGTGCT CAGAGGAGGT
GAGAGGAGAG GAAGGAGAAA ACTGCATCAT AACTTTACAG AATTGAATCT
AGAGTCTTCC CCGAAAAGCC CAGAAACTTC TCTGCAGTAT CTGGCTTGTC
CATCTGGTCT AAGGTGGCTG CTTCTTCCCC AGCCATGAGT CAGTTTGTGC
CCATGAATAA TACACGACCT GTTATTTCCA TGACTGCTTT ACTGTATTTT
TAAGGTCAAT ATACTGTACA TTTGATAATA AAATAATATT CTCCCAAAAA AAAAA

Figure 53 **Human OCP: nucleotide sequence of ORF**

ATGAAGGTAAAAGGCAGAGGAATCACCTGCTTGCTGGTCTCCTTTGCTGTGATCTGC
CTGGTCGCCACCCCTGGGGGCAAGGCCTGTCCTCGCCGCTGTGCCTGTTATATGCCT
ACGGAGGTACACTGCACATTTCGGTACCTGACTTCCATCCCAGACAGCATCCCGCCC
AATGTGGAACGCATCAATTTAGGATACAACAGCTTGGTTAGATTGATGGAAACAGAT
TTTTCTGGCCTGACCAAACTGGAGTTACTCATGCTTCACAGCAATGGCATTCACACA
ATCCCTGACAAGACCTTCTCAGATTTGCAGGCCTTGCAGGTCTTAAAAATGAGCTAT
AATAAAGTCCGAAAACTTCAGAAAGATACTTTTTATGGCCTCAGGAGCTTGACACGA
TTGCACATGGACCACAACAATATTGAGTTTATAAACCCAGAGGTTTTTTATGGGCTC
AACTTTCTCCGCCTGGTGCACTTGGAAGGAAATCAGCTCACTAAGCTCCACCCAGAT
ACATTTGTCTCTTTGAGCTACCTCCAGATATTTAAAATCTCTTTCATTAAGTTCCTA
TACTTGTCTGATAACTTCCTGACCTCCCTCCCTCAAGAGATGGTCTCCTATATGCCT
GACCTAGACAGCCTTTACCTGCATGGAAACCCATGGACCTGTGATTGCCATTTAAAG
TGGTTGTCTGACTGGATACAGGAGAAGCCAGATGTAATAAAATGCAAAAAAGATAGA
AGTCCCTCTAGTGCTCAGCAGTGTCCACTTTGCATGAACCCTAGGACTTCTAAAGGC
AAGCCGTTAGCTATGGTCTCAGCTGCAGCTTTCCAGTGTGCCAAGCCAACCATTGAC
TCATCCCTGAAATCAAAGAGCCTGACTATTCTGGAAGACAGTAGTTCTGCTTTCATC
TCTCCCCAAGGTTTCATGGCACCCTTTGGCTCCCTCACTTTGAATATGACAGATCAG
TCTGGAAATGAAGCTAACATGGTCTGCAGTATTCAAAAGCCCTCAAGGACATCACCC
ATTGCATTCACTGAAGAAAATGACTACATCGTGCTAAATACTTCATTTTCAACATTT
TTGGTGTGCAACATAGATTACGGTCACATTCAGCCAGTGTGGCAAATTTTGGCTTTG
TACAGTGATTCTCCTCTGATACTAGAAAGGAGCCACTTGCTTAGTGAAACACCGCAG
CTCTATTACAAATATAAACAGGTGGCTCCTAAGCCTGAAGACATTTTTACCAACATA
GAGGCAGATCTCAGAGCAGATCCCTCTTGGTTAATGCAAGACCAAATTTCCTTGCAG
CTGAACAGAACTGCCACCACATTCAGTACATTACAGATCCAGTACTCCAGTGATGCT
CAAATCACTTTACCAAGAGCAGAGATGAGGCCAGTGAAACACAAATGGACTATGATT
TCAAGGGATAACAATACTAAGCTGGAACATACTGTCTTGGTAGGTGGAACCGTTGGC
CTGAACTGCCCAGGCCAAGGAGACCCCACCCCACACGTGGATTGGCTTCTAGCTGAT
GGAAGTAAAGTGAGAGCCCCTTATGTCAGTGAGGATGGACGGATCCTAATAGACAAA
AGTGGAAAATTGGAACTCCAGATGGCTGATAGTTTTGACACAGGCGTATATCACTGT
ATAAGCAGCAATTATGATGATGCAGATATTCTCACCTATAGGATAACTGTGGTAGAA
CCTTTGGTCGAAGCCTATCAGGAAAATGGGATTCATCACACAGTTTTCATTGGTGAA
ACACTTGATCTTCCATGCCATTCTACTGGTATCCCAGATGCCTCTATTAGCTGGGTT
ATTCCAGGAAACAATGTGCTCTATCAGTCATCAAGAGACAAGAAAGTTCTAAACAAT
GGCACATTAAGAATATTACAGGTCACCCCGAAAGACCAAGGTTATTATCGCTGTGTG
GCAGCCAACCCATCAGGGGTTGATTTTTTGATTTTCCAAGTTTCAGTCAAGATGAAA
GGACAAAGGCCCTTGGAGCATGATGGAGAAACAGAGGGATCTGGACTTGATGAGTCC
AATCCTATTGCTCATCTTAAGGAGCCACCAGGTGCACAACTCCGTACATCTGCTCTG
ATGGAGGCTGAGGTTGGAAAACACACCTCAAGCACAAGTAAGAGGCACAACTATCGG
GAATTAACACTCCAGCGACGTGGAGATTCAACACATCGACGTTTTAGGGAGAATAGG
AGGCATTTCCCTCCCTCTGCTAGGAGAATTGACCCACAACATTGGGCGGCACTGTTG
GAGAAAGCTAAAAAGAATGCTATGCCAGACAAGCGAGAAAATACCACAGTGAGCCCA
CCCCCAGTGGTCACCCAACTCCCAAACATACCTGGTGAAGAAGACGATTCCTCAGGC
ATGCTCGCTCTACATGAGGAATTTATGGTCCCGGCCACTAAAGCTTTGAACCTTCCA
GCAAGGACAGTGACTGCTGACTCCAGAACAATATCTGATAGTCCTATGACAAACATA
AATTATGGCACAGAATTCTCTCCTGTTGTGAATTCACAAATACTACCACCTGAAGAA
CCCACAGATTTCAAACTGTCTACTGCTATTAAAACTACAGCCATGTCAAAGAATATA

AACCCAACCATGTCAAGCCAAATACAAGGCACAACCAATCAACATTCATCCACTGTC
TTTCCACTGCTACTTGGAGCAACTGAATTTCAGGACTCTGACCAGATGGGAAGAGGA
AGAGAGCATTTCCAAAGTAGACCCCCAATAACAGTAAGGACTATGATCAAAGATGTC
AATGTCAAAATGCTTAGTAGCACCACCAACAAACTATTATTAGAGTCAGTAAATACC
ACAAATAGTCATCAGACATCTGTAAGAGAAGTGAGTGAACCCAGGCACAATCACTTC
TATTCTCACACTACTCAAATACTTAGCACCTCCACGTTCCCTTCAGATCCACACACA
GCTGCTCATTCTCAGTTTCCGATCCCTAGAAATAGTACAGTTAACATCCCGCTGTTC
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AGAACTCCAGTTCTGCGACGGCATAGATACAGCATTTTCAGGTCAACAACCAGAGGT
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TCCTGTCTTCCCAGGGAGAGGCTCACCACTGCCACAGCAGCATTGTCTTTTCCAAGT
GCTGCTCCCATCACCTTCCCCAAAGCTGACATTGCTAGAGTCCCATCAGAAGAGTCT
ACAACTCTAGTCCAGAATCCACTATTACTACTTGAGAACAAACCCAGTGTAGAGAAA
ACAACACCCACAATAAAATATTTCAGGACTGAAATTTCCCAAGTGACTCCAACTGGT
GCAGTCATGACATATGCTCCAACATCCATACCCATGGAAAAAACTCACAAAGTAAAC
GCCAGTTACCCACGTGTGTCTAGCACCAATGAAGCTAAAAGAGATTCAGTGATTACA
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TTTTCAAGAAGGAAAATTCCCTGGCAACAGAACTTTGTAAATAACCATAACCCAAAA
GGCAGATTAAGGAATCAACATAAAGTTAGTTTACAAAAAAGCACAGCTGTGATGCTT
CCTAAAACATCTCCTGCTTTACCACAGAGACAAAGTTCCCCTTTCCATTTCACCACA
CTTTCAACAAGTGTGATGCAAATTCCATCTAATACCTTGACTACCGCTCACCACACT
ACGACCAAAACACACAATCCTGGAAGTCTTCCAACAAAGAAGGAGCTTCCCTTCCCA
CCCCTTAACCCTATGCTTCCTAGTATTATAAGCAAAGACTCAAGTACAAAAAGCATC
ATATCAACGCAAACAGCAATACCAGCAACAACTCCTACCTTCCCTGCATCTGTCATC
ACTTATGAAACCCAAACAGAGAGATCTAGAGCACAAACAATACAAAGAGAACAGGAG
CCTCAAAAGAAGAACAGGACTGACCCAAACATCTCTCCAGACCAGAGTTCTGGCTTC
ACTACACCCACTGCTATGACACCTCCTGCTCTGGCATTCACTCATTCCCCACCAGAA
AACACAACTGGGATTTCAAGCACAATCAGTTTTCATTCAAGAACTCTTAATCTGACA
GATGTGATTGAAGAACTAGCCCAAGCAAGTACTCAGACTTTGAAGAGCACAATTGCT
TCTGAAACAACTTTGTCCAGCAAATCACACCAGAGTACCACAACTAGGAAAGCATCA
TTAGACACTCCCATACCACCATTCTTGAGCAGCAGTGCTACTCTAATGCCAGTTCCC
ATCTCCCCTCCCTTTACTCAGAGAGCAGTTACTGACACACGTGGCGACTCCCATTTC
CGGCTTATGACAAATACAGTGGTCAAGCTGCACGAATCCTCAAGGCACAATCTCCAA
ATGCCAAGTTCACAATTGGAACCACTCACTTCATCTACCTCTAATCTGTTACATTCT
ACTCCCATGCCAGCACTAACAACAGTTAAATCACAGAATTCCAAATTAACTCCATCT
CCCTGGGCAGAATACCAATTTTGGCACAAACCATACTCAGACATTGCTGAAAAAGGC
AAAAAGCCAGAAGTAAGCATGTTGGCTACTACAGGCCTGTCCGAGGCCACCACTCTT
GTTTCAGATTGGGATGGACAGAAGAACACAAAGAAGAGTGACTTTGATAAGAAACCA
GTTCAAGAAGCAACAACTTCCAAACTCCTTCCCTTTGACTCTTTGTCTAGGTATATA
TTTGAAAAGCCCAGGATAGTTGGAGGAAAAGCTGCAAGTTTTACTATTCCAGCTAAC
TCAGATGCCTTTCTTCCCTGTGAAGCTGTTGGAAATCCCCTGCCCACCATTCATTGG
ACCAGAGTTTCAGGACTTGATTTATCTAGAGGAAACCAGAATAGCAGGGTCCAGGTT
CTCCCCAATGGTACCCTGTCCATCCAGAGGGTGGAAATTCAGGACCGCGGACAGTAC
TTGTGTTCCGCATCCAATCTGTTTGGCACAGACCACCTTCATGTCACCTTGTCTGTG
GTTTCCTATCCTCCCAGGATCCTGGAGAGACGTACCAAAGAGATCACAGTTCATTCC
GGAAGCACTGTGGAACTGAAGTGCAGAGCAGAAGGTAGGCCAAGCCCTACAGTTACC
TGGATTCTTGCAAACCAAACAGTTGTCTCAGAATCATCCCAGGGAAGTAGGCAGGCT
GTGGTGACGGTTGACGGAACATTGGTCCTCCACAATCTCAGTATTTATGACCGTGGC
TTTTACAAATGTGTGGCCAGCAACCCAGGTGGCCAGGATTCACTGCTGGTTAAAATA
CAAGTCATTGCAGCACCACCTGTTATTCTAGAGCAAAGGAGGCAAGTCATTGTAGGC
ACTTGGGGTGAAAGTTTAAAACTGCCCTGTACTGCAAAAGGAACTCCTCAGCCCAGC

GTTTACTGGGTCCTCTCTGATGGCACTGAAGTGAAACCATTACAGTTTACCAATTCC
AAGTTGTTCTTATTTTCAAATGGGACTTTGTATATAAGAAACCTAGCCTCTTCAGAC
AGGGGCACTTATGAATGCATTGCTACCAGTTCCACTGGTTCGGAGCGAAGAGTAGTA
ATGCTTACAATGGAAGAGCGAGTGACCAGCCCCAGGATAGAAGCTGCATCCCAGAAA
AGGACTGAAGTGAATTTTGGGGACAAATTACTACTGAACTGCTCAGCCACTGGGGAG
CCCAAACCCCAAATAATGTGGAGGTTACCATCCAAGGCTGTGGTCGACCAGTGGAGC
TGGATCCACGTCTACCCTAATGGATCCCTGTTTATTGGATCAGTAACAGAAAAAGAC
AGTGGTGTCTACTTGTGTGTGGCAAGAAACAAAATGGGGGATGATCTGATACTGATG
CATGTTAGCCTAAGACTGAAACCTGCCAAAATTGACCACAAGCAGTATTTTAGAAAG
CAAGTGCTCCATGGGAAAGATTTCCAAGTAGATTGCAAAGCTTCCGGCTCCCCAGTG
CCAGAGATATCTTGGAGTTTGCCTGATGGAACCATGATCAACAATGCAATGCAAGCC
GATGACAGTGGCCACAGGACTAGGAGATATACCCTTTTCAACAATGGAACTTTATAC
TTCAACAAAGTTGGGGTAGCGGAGGAAGGAGATTATACTTGCTATGCCCAGAACACC
CTAGGGAAAGATGAAATGAAGGTCCACTTAACAGTTATAACAGCTGCTCCCCGGATA
AGGCAGAGTAACAAAACCAACAAGAGAATCAAAGCTGGAGACACAGCTGTCCTTGAC
TGTGAGGTCACTGGGGATCCCAAACCAAAAATATTTTGGTTGCTGCCTTCCAATGAC
ATGATTTCCTTCTCCATTGATAGGTACACATTTCATGCCAATGGGTCTTTGACCATC
AACAAAGTGAAACTGCTCGATTCTGGAGAGTACGTATGTGTAGCCCGAAATCCCAGT
GGGGATGACACCAAAATGTACAAACTGGATGTGGTCTCTAAACCTCCATTAATCAAT
GGTCTGTATACAAACAGAACTGTTATTAAAGCCACAGCTGTGAGACATTCCAAAAAA
CACTTTGACTGCAGAGCTGAAGGGACACCATCTCCTGAAGTCATGTGGATCATGCCA
GACAATATTTTCCTCACAGCCCCATACTATGGAAGCAGAATCACAGTCCATAAAAAT
GGAACCTTGGAAATTAGGAATGTGAGGCTTTCAGATTCAGCCGACTTTATCTGTGTG
GCCCGAAATGAAGGTGGAGAGAGCGTGTTGGTAGTACAGTTAGAAGTACTGGAAATG
CTGAGAAGACCGACATTTAGAAATCCATTTAATGAAAAAATAGTTGCCCAGCTGGGA
AAGTCCACAGCATTGAATTGCTCTGTTGATGGTAACCCACCACCTGAAATAATCTGG
ATTTTACCAAATGGCACACGATTTTCCAATGGACCACAAAGTTATCAGTATCTGATA
GCAAGCAATGGTTCTTTTATCATTTCTAAAACAACTCGGGAGGATGCAGGAAAATAT
CGCTGTGCAGCTAGGAATAAAGTTGGCTATATTGAGAAATTAGTCATATTAGAAATT
GGCCAGAAGCCAGTTATTCTTACCTATGCACCAGGGACAGTAAAAGGCATCAGTGGA
GAATCTCTATCACTGCATTGTGTGTCTGATGGAATCCCTAAGCCAAATATCAAATGG
ACTATGCCAAGTGGTTATGTAGTAGACAGGCCTCAAATTAATGGGAAATACATATTG
CATGACAATGGCACCTTAGTCATTAAAGAAGCAACAGCTTATGACAGAGGAAACTAT
ATCTGTAAGGCTCAAAATAGTGTTGGTCATACACTGATTACTGTTCCAGTAATGATT
GTAGCCTACCCTCCCCGAATTACAAATCGTCCACCCAGGAGTATTGTCACCAGGACA
GGGGCAGCCTTTCAGCTCCACTGTGTGGCCTTGGGAGTTCCCAAGCCAGAAATCACA
TGGGAGATGCCTGACCACTCCCTTCTCTCAACGGCAAGTAAAGAGAGGACACATGGA
AGTGAGCAGCTTCACTTACAAGGTACCCTAGTCATTCAGAATCCCCAAACCTCCGAT
TCTGGGATATACAAATGCACAGCAAAGAACCCACTTGGTAGTGATTATGCAGCAACG
TATATTCAAGTAATCTGA

Figure 54 **Human OCP: predicted amino acid sequence**

MKVKGRGITC LLVSFAVICL VATPGGKACP RRCACYMPTE VHCTFRYLTS
IPDSIPPNVE RINLGYNSLV RLMETDFSGL TKLELLMLHS NGIHTIPDKT
FSDLQALQVL KMSYNKVRKL QKDTFYGLRS LTRLHMDHNN IEFINPEVFY
GLNFLRLVHL EGNQLTKLHP DTFVSLSYLQ IFKISFIKFL YLSDNFLTSL
PQEMVSYMPD LDSLYLHGNP WTCDCHLKWL SDWIQEKPDV IKCKKDRSPS
SAQQCPLCMN PRTSKGKPLA MVSAAAFQCA KPTIDSSLKS KSLTILEDSS
SAFISPQGFM APFGSLTLNM TDQSGNEANM VCSIQKPSRT SPIAFTEEND
YIVLNTSFST FLVCNIDYGH IQPVWQILAL YSDSPLILER SHLLSETPQL
YYKYKQVAPK PEDIFTNIEA DLRADPSWLM QDQISLQLNR TATTFSTLQI
QYSSDAQITL PRAEMRPVKH KWTMISRDNN TKLEHTVLVG GTVGLNCPGQ
GDPTPHVDWL LADGSKVRAP YVSEDGRILI DKSGKLELQM ADSFDTGVYH
CISSNYDDAD ILTYRITVVE PLVEAYQENG IHHTVFIGET LDLPCHSTGI
PDASISWVIP GNNVLYQSSR DKKVLNNGTL RILQVTPKDQ GYYRCVAANP
SGVDFLIFQV SVKMKGQRPL EHDGETEGSG LDESNPIAHL KEPPGAQLRT
SALMEAEVGK HTSSTSKRHN YRELTLQRRG DSTHRRFREN RRHFPPSARR
IDPQHWAALL EKAKKNAMPD KRENTTVSPP PVVTQLPNIP GEEDDSSGML
ALHEEFMVPA TKALNLPART VTADSRTISD SPMTNINYGT EFSPVVNSQI
LPPEEEPTDFK LSTAIKTTAM SKNINPTMSS QIQGTTNQHS STVFPLLLGA
TEFQDSDQMG RGREHFQSRP PITVRTMIKD VNVKMLSSTT NKLLLESVNT
TNSHQTSVRE VSEPRHNHFY SHTTQILSTS TFPSDPHTAA HSQFPIPRNS
TVNIPLFRRF GRQRKIGGRG RIISPYRTPV LRRHRYSIFR STTRGSSEKS
TTAFSATVLN VTCLSCLPRE RLTTATAALS FPSAAPITFP KADIARVPSE
ESTTLVQNPL LLLENKPSVE KTTPTIKYFR TEISQVTPTG AVMTYAPTSI
PMEKTHKVNA SYPRVSSTNE AKRDSVITSS LSGAITKPPM TIIAITRFSR
RKIPWQQNFV NNHNPKGRLR NQHKVSLQKS TAVMLPKTSP ALPQRQSSPF
HFTTLSTSVM QIPSNTLTTA HHTTTKTHNP GSLPTKKELP FPPLNPMLPS
IISKDSSTKS IISTQTAIPA TTPTFPASVI TYETQTERSR AQTIQREQEP
QKKNRTDPNI SPDQSSGFTT PTAMTPPALA FTHSPPENTT GISSTISFHS
RTLNLTDVIE ELAQASTQTL KSTIASETTL SSKSHQSTTT RKASLDTPIP
PFLSSSATLM PVPISPPFTQ RAVTDTRGDS HFRLMTNTVV KLHESSRHNL
QMPSSQLEPL TSSTSNLLHS TPMPALTTVK SQNSKLTPSP WAEYQFWHKP
YSDIAEKGKK PEVSMLATTG LSEATTLVSD WDGQKNTKKS DFDKKPVQEA
TTSKLLPFDS LSRYIFEKPR IVGGKAASFT IPANSDAFLP CEAVGNPLPT
IHWTRVSGLD LSRGNQNSRV QVLPNGTLSI QRVEIQDRGQ YLCSASNLFG
TDHLHVTLSV VSYPPRILER RTKEITVHSG STVELKCRAE GRPSPTVTWI
LANQTVVSES SQGSRQAVVT VDGTLVLHNL SIYDRGFYKC VASNPGGQDS
LLVKIQVIAA PPVILEQRRQ VIVGTWGESL KLPCTAKGTP QPSVYWVLSD
GTEVKPLQFT NSKLFLFSNG TLYIRNLASS DRGTYECIAT SSTGSERRVV
MLTMEERVTS PRIEAASQKR TEVNFGDKLL LNCSATGEPK PQIMWRLPSK
AVVDQWSWIH VYPNGSLFIG SVTEKDSGVY LCVARNKMGD DLILMHVSLR
LKPAKIDHKQ YFRKQVLHGK DFQVDCKASG SPVPEISWSL PDGTMINNAM
QADDSGHRTR RYTLFNNGTL YFNKVGVAEE GDYTCYAQNT LGKDEMKVHL
TVITAAPRIR QSNKTNKRIK AGDTAVLDCE VTGDPKPKIF WLLPSNDMIS
FSIDRYTFHA NGSLTINKVK LLDSGEYVCV ARNPSGDDTK MYKLDVVSKP
PLINGLYTNR TVIKATAVRH SKKHFDCRAE GTPSPEVMWI MPDNIFLTAP
YYGSRITVHK NGTLEIRNVR LSDSADFICV ARNEGGESVL VVQLEVLEML
RRPTFRNPFN EKIVAQLGKS TALNCSVDGN PPPEIIWILP NGTRFSNGPQ
SYQYLIASNG SFIISKTTRE DAGKYRCAAR NKVGYIEKLV ILEIGQKPVI

LTYAPGTVKG ISGESLSLHC VSDGIPKPNI KWTMPSGYVV DRPQINGKYI
LHDNGTLVIK EATAYDRGNY ICKAQNSVGH TLITVPVMIV AYPPRITNRP
PRSIVTRTGA AFQLHCVALG VPKPEITWEM PDHSLLSTAS KERTHGSEQL
HLQGTLVIQN PQTSDSGIYK CTAKNPLGSD YAATYIQVI*